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## **RESPONSE**

### **I. Status of the Claims**

No claims have been cancelled. Claims 1-3 have been amended. New claims 4-22 have been added.

Claims 1-22 are therefore presently pending in the case.

### **II. Support for the Amended and Newly Added Claims**

Claims 1 and 2 have been amended to correct clerical errors. Support for this claim can be found throughout the specification as originally filed, with particular support being found at least in claims 1 and 2 as originally filed.

Claim 3 has been amended to recite expression vectors that encode the amino acid sequence shown in SEQ ID NO:2, SEQ ID NO:4 or SEQ ID NO:6. Support for this claim can be found throughout the specification as originally filed, with particular support being found at least from page 14, line 32 to page 15, line 6, and in claim 3 as originally filed.

Claims 4-6 have been added to specifically recite the alternative embodiments of claim 1.

Claims 7-9 have been added to specifically recite the alternative embodiments of claim 2.

Claims 10-15 have been added to specifically recite the alternative embodiments of claim 3.

Claims 16-22 have been added to specifically recite host cells comprising the expression vector of claim 3, and the alternate embodiments therein. Support for these claims can be found throughout the specification as originally filed, with particular support being found at least at page 15, lines 6-12.

It will be understood that no new matter is included within the amended or newly added claims.

### **III. Rejection of Claims 1-3 Under 35 U.S.C. § 101**

The Action next rejects claims 1-3 under 35 U.S.C. § 101, as allegedly lacking a patentable utility. Applicants respectfully traverse.

The present invention has a number of substantial and credible utilities, not the least of which is in forensic biology, as described in the specification, at least at page 3, lines 11-13. As described in the specification at page 18, lines 18-22, an A/G coding single nucleotide polymorphism was identified at nucleotide position 4079 of SEQ ID NO:1, 4454 of SEQ ID NO:3 and 4502 of SEQ ID

NO:5, which can result in either a lysine or arginine being present at corresponding amino acid position 1360 of SEQ ID NO:2, 1485 of SEQ ID NO:4, or 1501 of SEQ ID NO:6, respectively. As such polymorphisms are the basis for forensic analysis, which is undoubtedly a “real world” utility, the presently claimed sequence must in itself be useful. Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101.

The Examiner questions this asserted utility, stating that “there is no evidence that the claimed polynucleotides have sequences that vary from person to person that would allow such an identification” (the Action at page 5). Applicants respectfully disagree, and point out that as described in the specification at page 18, lines 18-22, the presently claimed sequences do in fact define a coding single nucleotide polymorphism. Polymorphisms are **by definition** “sequences that vary from person to person”. Thus, as the Examiner’s argument is completely without merit, the present claims clearly meet the requirements of 35 U.S.C. § 101.

The Examiner further questions this asserted utility because “neither the Specification nor the art of record disclose any diseases or conditions related to the proteins encoded by the polynucleotides of the invention” (the Action at page 3). First, Applicants respectfully point out that the identification of “any diseases or conditions related to the proteins encoded by the polynucleotides of the invention” is not the standard for patentability under 35 U.S.C. § 101 (*In re Brana*, 34 USPQ2d 1436 (Fed. Cir. 1995)). Second, Applicants respectfully point out that the use of the presently described polymorphisms in forensic analysis does **not** require the identification of a specific medical condition. One aspect of forensic analysis is to distinguish individual members of the human population from one another based solely on the **presence** or **absence** of a polymorphic marker, such as the presently described polymorphism. As polymorphic markers such as the presently described polymorphism have been used in forensic analysis for decades, this is clearly a well established technique, and as such, specific guidance does not need to be provided in the present specification, for it has long been established that a patent need not disclose what is well known in the art (*In re Wands*, 8 USPQ 2d 1400 (Fed. Cir. 1988)). This is also not a case of a “potential” utility. Using the polymorphic marker exactly as described in the specification as originally filed, the skilled artisan can in fact distinguish individuals from one another. Applicants point out that in the **worst case** scenario, the marker is useful to distinguish 50% of the population (in other words, the marker being present in half of the population). This is an inherent feature of any polymorphic marker, as the largest percentage of a population that two

polymorphic markers can define is 50% each. If a polymorphic marker is present at a level of less than 50%, then that marker is even **more** informative, *i.e.*, a **greater** percentage of the population can be distinguished on the basis of the marker. Nevertheless, the ability to eliminate even 50% of the population from a forensic analysis clearly is a real world, practical utility.

The Examiner next states that “(a) ‘substantial’ utility is a utility that defines a ‘real world’ use” (the Action at page 3). Applicants respectfully point out that naturally occurring genetic polymorphisms such as those described in the specification as originally filed are both the basis of, and critical to, *inter alia*, forensic genetic analysis intended to resolve issues of, for example, identity or paternity. Forensic analysis based on polymorphisms such as that identified by Applicants is used to positively identify or rule out suspects in many criminal cases, and in identifying human remains. Paternity determination is based on polymorphisms such as that identified by Applicants to positively identify or rule out individuals suspected of fathering a particular child. What could be possibly be more “substantial” and “real world” than the loss of an individual’s freedom or life through incarceration? What could be possibly be more “substantial” and “real world” than the positive identification of human remains? What could be possibly be more “substantial” and “real world” than the impact, both economic and emotional, that the results of a paternity analysis has on the individuals directly and indirectly involved? These are all well known and generally accepted uses of polymorphisms such as the polymorphism identified by Applicants. Without such identified polymorphisms, the skilled artisan would not be able to carry out such forensic or paternal analyses. Therefore, as the use of the presently described polymorphic marker in forensic analysis is clearly a “substantial” and “real world” utility, the presently claimed sequences meet the requirements of 35 U.S.C. § 101.

The Examiner further questions this asserted utility, stating that “further research would be required to reasonably confirm or identify how the polynucleotides could be used in such assays” (the Action at page 5). Applicants reiterate that the use of the presently described polymorphic marker in forensic analysis, as detailed above, requires **no** further research. The presently described polymorphism can be used to distinguish individuals from one another in their presently available form. Furthermore, Applicants take this opportunity to note that throughout the Action the Examiner repeatedly cites the need for “further research” (the Action at least at pages 3 (three times) and 5) to support the allegation that the present invention lacks a patentable utility. Applicants respectfully point out that the proper standard for meeting the requirements of 35 U.S.C. § 101 is **not** whether “further

research” is required to practice certain aspects of the claimed invention, but whether undue experimentation would be required to practice the claimed invention. The widespread use of polymorphisms such as that described by Applicants in forensic analysis every day strongly argues against such a use requiring “undue experimentation”. Applicants reiterate that in assessing the question of whether undue experimentation would be required in order to practice the claimed invention, the key term is “undue”, not “experimentation”. *In re Angstadt and Griffin*, 190 USPQ 214 (CCPA 1976). The need for some experimentation does not render the claimed invention unpatentable. Indeed, a considerable amount of experimentation may be permissible if such experimentation is routinely practiced in the art. *In re Angstadt and Griffin, supra*; *Amgen, Inc. v. Chugai Pharmaceutical Co., Ltd.*, 18 USPQ2d 1016 (Fed. Cir. 1991). Thus, the Examiner’s argument once again does not support the alleged lack of utility, and the present claims clearly meet the requirements of 35 U.S.C. § 101.

The Examiner goes on to state that this asserted utility are “not considered specific” because “any nucleic acid molecule could be used” in this fashion, and thus the utility is considered “general” (the Action bridging pages 2 and 3). Applicants first point out that not all nucleic acids contain polymorphic markers. In fact, the basis for forensic analysis is the fact that such polymorphic markers are not present in all other nucleic acids, but in fact specific and unique to only a certain subset of the population. Second, until a polymorphic marker is actually described it cannot be used in forensic analysis. Put another way, simply because there is a likelihood, even a significant likelihood, that a particular nucleic acid sequence will contain a polymorphism and thus be useful in forensic analysis, until such a polymorphism is actually identified and described, such a likelihood is meaningless. Third, the Examiner appears to be confusing the requirement for a specific utility, which is the proper standard for utility under 35 U.S.C. § 101, with the requirement for a unique utility, which is clearly an improper standard. As set forth by the Federal Circuit in *Carl Zeiss Stiftung v. Renishaw PLC*, 20 USPQ2d 1101 (Fed. Cir. 1991; “*Carl Zeiss*”):

An invention need not be the best or only way to accomplish a certain result, and it need only be useful to some extent and in certain applications: “[T]he fact that an invention has only limited utility and is only operable in certain applications is not grounds for finding a lack of utility.” *Envirotech Corp. v. Al George, Inc.*, 221 USPQ 473, 480 (Fed. Cir. 1984)

Following directly from the quote above, an invention does not need to be the only way to accomplish

a certain result. Thus, the question of whether or not other nucleic acid sequences contain polymorphic markers and can thus be used in forensic analysis is completely irrelevant to the present utility inquiry. The only relevant question in regard to meeting the standards of 35 U.S.C. § 101 is whether every nucleic acid can be so used - and the clear answer to this question is an emphatic no. Importantly, the holding in the *Carl Zeiss* case is mandatory legal authority that essentially controls the outcome of the present case. This case, and particularly the cited quote, directly rebuts the Examiner's argument. Furthermore, the requirement for a unique utility is clearly not the standard adopted by the United States Patent and Trademark Office ("the USPTO"). If every invention were required to have a unique utility, the USPTO would no longer be issuing patents on batteries, automobile tires, golf balls, golf clubs, and treatments for a variety of human diseases, such as cancer and bacterial or viral infections, just to name a few particular examples, because examples of each of these have already been described and patented. All batteries have the exact same utility - specifically, to provide power. All automobile tires have the exact same utility - specifically, for use on automobiles. All golf balls and golf clubs have the exact same utility - specifically, use in the game of golf. All cancer treatments have the exact same utility - specifically, to treat cancer. All anti-infectious agents have the exact same broader utility - specifically, to treat infections. However, only the briefest perusal of virtually any issue of the Official Gazette provides numerous examples of patents being granted on each of the above compositions every week. Additionally, if a composition needed to be unique to be patented, the entire class and subclass system would be an effort in futility, as the class and subclass system serves solely to group such common inventions, which would not be required if each invention needed to have a unique utility. Thus, the present sequence clearly meets the requirements of 35 U.S.C. § 101.

Throughout the Action, the Examiner attempts to narrowly define the "general" class of the invention to include only those members that share the asserted utility, and then state that the asserted utility is "general". Applicants respectfully point out that the "general" class with regard to the present invention is all nucleic acids. Applicants reiterate that not all nucleic acids contain polymorphisms. Therefore, the question of whether the asserted utility is "specific", as opposed to "general", has clearly been laid to rest. Applicants note that the "general" class of the invention cannot be redefined to include only those nucleic acids that contain polymorphic markers, as the Examiner is forced to do in order to support the allegation that the claimed nucleic acids lack a patentable utility. Thus, the Examiner's argument is completely improper and in clear defiance of established case law, and therefore is in no

way whatsoever sufficient to overcome Applicants' assertion of utility. Therefore the present claims are clearly in compliance with 35 U.S.C. § 101.

Furthermore, Applicants point out that as the presently described polymorphisms are part of the family of polymorphisms that have a well established utility, the Federal Circuit's holding in *In re Brana* (*supra*; "*Brana*") is directly on point. In *Brana*, the Federal Circuit admonished the Patent and Trademark Office for confusing "the requirements under the law for obtaining a patent with the requirements for obtaining government approval to market a particular drug for human consumption". *Brana* at 1442. The Federal Circuit went on to state:

At issue in this case is an important question of the legal constraints on patent office examination practice and policy. The question is, with regard to pharmaceutical inventions, what must the applicant provide regarding the practical utility or usefulness of the invention for which patent protection is sought. This is not a new issue; it is one which we would have thought had been settled by case law years ago.

*Brana* at 1439, emphasis added. The choice of the phrase "utility or usefulness" in the foregoing quotation is highly pertinent. The Federal Circuit is evidently using "utility" to refer to rejections under 35 U.S.C. § 101, and is using "usefulness" to refer to rejections under 35 U.S.C. § 112, first paragraph. This is made evident in the continuing text in *Brana*, which explains the correlation between 35 U.S.C. §§ 101 and 112, first paragraph. The Federal Circuit concluded:

FDA approval, however, is not a prerequisite for finding a compound useful within the meaning of the patent laws. Usefulness in patent law, and in particular in the context of pharmaceutical inventions, necessarily includes the expectation of further research and development. The stage at which an invention in this field becomes useful is well before it is ready to be administered to humans. Were we to require Phase II testing in order to prove utility, the associated costs would prevent many companies from obtaining patent protection on promising new inventions, thereby eliminating an incentive to pursue, through research and development, potential cures in many crucial areas such as the treatment of cancer.

*Brana* at 1442-1443, citations omitted, emphasis added.

Additionally, it is important to note that it has been clearly established that a statement of utility in a specification must be accepted absent reasons why one skilled in the art would have reason to doubt the objective truth of such statement. *In re Langer*, 503 F.2d 1380, 1391, 183 USPQ 288, 297 (CCPA, 1974; "*Langer*"); *In re Marzocchi*, 439 F.2d 220, 224, 169 USPQ 367, 370 (CCPA, 1971). As clearly set forth in *Langer*:

As a matter of Patent Office practice, a specification which contains a disclosure of utility which corresponds in scope to the subject matter sought to be patented must be taken as sufficient to satisfy the utility requirement of § 101 for the entire claimed subject matter unless there is a reason for one skilled in the art to question the objective truth of the statement of utility or its scope.

*Langer* at 297, emphasis in original. As set forth in the MPEP, “Office personnel must provide evidence sufficient to show that the statement of asserted utility would be considered ‘false’ by a person of ordinary skill in the art” (MPEP, Eighth Edition at 2100-40, emphasis added). Absent such evidence from the Examiner, as the skilled artisan would readily understand that the present polymorphic markers have utility in forensic analysis, the present claims clearly meet the requirements of 35 U.S.C. § 101.

The Examiner states that “a sequence search did not reveal any sequences identical or related to the sequences of the present invention that were known at the time of the invention”, and “(t)herefore, at the time of the invention the art did not teach or suggest that the proteins encoded by the polynucleotides with similar sequence to those of the present invention were related to any disease or disorder” (the Action at page 4). First, Applicants readily agree that no “sequences identical . . . to the sequences of the present invention” are present in the prior art, since such a sequence would completely anticipate the present invention. Applicants respectfully point out that no rejection under any subsection of 35 U.S.C. § 102 has been entered against the present claims, confirming this fact. Second, Applicants point out that whether or not the sequences of the present invention “were related to any disease or disorder” is not the standard for patentability under 35 U.S.C. § 101 (*In re Brana, supra*). Thus, these arguments by the Examiner also in no way supports the alleged lack of utility.

It has been well established that Applicants need only make one credible assertion of utility to meet the requirements of 35 U.S.C. § 101 (*Raytheon v. Roper*, 220 USPQ 592 (Fed. Cir. 1983); *In re Gottlieb*, 140 USPQ 665 (CCPA 1964); *In re Malachowski*, 189 USPQ 432 (CCPA 1976); *Hoffman v. Klaus*, 9 USPQ2d 1657 (Bd. Pat. App. & Inter. 1988)), and, thus, any questions concerning whether or not the present claims meet the requirements of 35 U.S.C. § 101 have already been laid to rest. Nevertheless, the present invention has a number of additional substantial and credible utilities, not the least of which is the utility of tracking expression of the presently claimed sequence. The specification details, at least at page 6, lines 12-14, that the present nucleotide sequences have utility in assessing gene expression patterns using high-throughput DNA chips. Such “DNA chips” clearly have utility, as evidenced by hundreds of issued U.S. Patents, as exemplified by



U.S. Patent Nos. 5,445,934, 5,556,752, 5,744,305, 5,837,832, 6,156,501 and 6,261,776 (**Exhibits A-F**; copies of issued U.S. Patents not provided pursuant to requests from the USPTO). As the present sequences are specific markers of human chromosome 2 (see below), those of skill in the art would instantly recognize that the present nucleotide sequences would be an ideal, novel candidate for assessing gene expression using such DNA chips. Given the widespread utility of such "gene chip" methods using *public domain* gene sequence information, there can be little doubt that the use of the presently described *novel* sequences would have great utility in such DNA chip applications. Clearly, compositions that enhance the utility of such DNA chips, such as the presently claimed nucleotide sequences, must in themselves be useful.

Further evidence of the "real world" substantial utility of the present invention is further provided by the fact that there is an entire industry established based on the use of gene sequences or fragments thereof in a gene chip format. Perhaps the most notable gene chip company is Affymetrix. However, there are many companies which have, at one time or another, concentrated on the use of gene sequences or fragments, in gene chip and non-gene chip formats, for example: Gene Logic, ABI-Perkin-Elmer, HySeq and Incyte. In addition, one such company (Rosetta Inpharmatics) was viewed to have such "real world" value that it was acquired by large a pharmaceutical company (Merck) for significant sums of money (net equity value of the transaction was \$620 million). The "real world" substantial industrial utility of gene sequences or fragments would, therefore, appear to be widespread and well established. Clearly, persons of skill in the art, as well as venture capitalists and investors, readily recognize the utility, both scientific and commercial, of genomic data in general, and specifically human genomic data. Billions of dollars have been invested in the human genome project, resulting in useful genomic data (see, *e.g.*, Venter *et al.*, *Science* **291**:1304, 2001; **Exhibit G**). The results have been a stunning success as the utility of human genomic data has been widely recognized as a great gift to humanity (see, *e.g.*, Jasny and Kennedy, *Science* **291**:1153, 2001; **Exhibit H**). Clearly, the usefulness of human genomic data, such as the presently claimed nucleic acid molecules, is substantial and credible (worthy of billions of dollars and the creation of numerous companies focused on such information) and well-established (the utility of human genomic information has been clearly understood for many years). Thus, the present sequence clearly meets the requirements of 35 U.S.C. § 101.

Regarding the implication that "any nucleic acid molecule" (the Action bridging pages 2 and 3)

could be so used, Applicants first point out that only expressed sequences can be used to assess gene expression patterns using DNA chips, not just any nucleic acid. Applicants reiterate that the requirements of a specific utility, which is the proper standard for utility under 35 U.S.C. § 101, should not be confused with the requirement for a unique utility, which is clearly an improper standard (*Carl Zeiss Stiftung v. Renishaw PLC, supra*). The fact that other nucleotide sequences are expressed and could thus be used to assess gene expression patterns using DNA chips does not mean that this use of Applicants' sequence is not a specific utility. Once again, the question of whether or not other nucleic acid sequences can be so used is completely irrelevant to the present utility inquiry. The only relevant question in regard to meeting the standards of 35 U.S.C. § 101 is whether every nucleic acid can be so used - and the clear answer to this question is once again an emphatic no. Applicants respectfully point out that in this case the Examiner is attempting to narrow the broad class of "any nucleic acid molecule" to include only those nucleic acid molecules that are expressed in order to support the allegation that the claimed nucleic acids lack a patentable utility, which Applicants point out once again is improper under the law as well as the policy of the USPTO. Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101.

As yet a further example of the utility of the presently claimed polynucleotide, as described in the specification at least at page 3, lines 3-5, the present nucleotide sequences have a specific utility in "identification of coding sequence" and "mapping a unique gene to a particular chromosome". The Examiner also questions these asserted utilities, stating "the Specification is no more specific than citing chromosome 2", and that "(s)uch is a general statement and does not include specifics such as where on chromosome 2 one would want to look" (the Action at page 5). Applicants respectfully disagree, and point out that as described in the specification as originally filed at page 3, lines 6-8, the gene encoding the presently claimed sequences is present on "human chromosome 2, see GENBANK accession no. AC011231". Thus, clearly, the specification as originally filed does include "specifics such as where on chromosome 2 one would want to look", specifically, the region of human chromosome 2 defined by GenBank Accession Number AC011231. In fact, alignment of SEQ ID NOS:1, 3 and 5 with GenBank Accession Number AC011231, as well as GenBank Accession Numbers AC019067, AC012000, AC016679, AC017082, and AC010873 (which are genomic clones from human chromosome 2 that overlap with AC011231) shows that the human gene

corresponding to SEQ ID NOS:1, 3 and 5 is dispersed on 26, 27, and 27, respectively, exons of human chromosome 2 (alignment and first pages of the GenBank reports are presented in **Exhibit I**). Clearly, the present polynucleotide provides exquisite specificity in localizing the specific region of human chromosome 2 that contains the gene encoding the given polynucleotide, a utility not shared by virtually any other nucleic acid sequences. In fact, it is this specificity that makes this particular sequence so useful. Early gene mapping techniques relied on methods such as Giemsa staining to identify regions of chromosomes. However, such techniques produced genetic maps with a resolution of only 5 to 10 megabases, far too low to be of much help in identifying specific genes involved in disease. The skilled artisan readily appreciates the significant benefit afforded by markers that map a specific locus of the human genome, such as the present nucleic acid sequence. For further evidence in support of the Applicants' position, the Examiner is requested to review, for example, section 3 of Venter *et al.* (*supra*, at pp. 1317-1321, including Fig. 11 at pp.1324-1325; see **Exhibit G**), which demonstrates the significance of expressed sequence information in the structural analysis of genomic data. The presently claimed polynucleotide sequence defines a biologically validated sequence that provides a unique and specific resource for mapping the genome essentially as described in the Venter *et al.* article. Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101.

Applicants point out that only a minor percentage (2-4%) of the genome actually encodes exons, which in-turn encode amino acid sequences. Equally significant is that the claimed polynucleotide sequence defines how the encoded exons are actually spliced together to produce an active transcript (*i.e.*, the described sequences are useful for functionally defining exon splice-junctions). As described in the specification as originally filed at page 3, lines 8-11, the claimed sequences "identify actual, biologically verified, and therefore relevant, exon splice junctions as opposed to those that may have been bioinformatically predicted from genomic sequence alone". The specification also details that "sequences derived from regions adjacent to the intron/exon boundaries of the human gene can be used to design primers for use in amplification assays to detect mutations within the exons, introns, splice sites (*e.g.*, splice acceptor and/or donor sites), *etc.*, that can be used in diagnostics and pharmacogenomics" (specification at page 11, lines 27-33). Applicants respectfully submit that the practical scientific value of biologically validated, expressed, spliced, and polyadenylated mRNA sequences is readily apparent to those skilled in the relevant biological and biochemical arts. Thus, the present sequence clearly meets

the requirements of 35 U.S.C. § 101.

Once again, regarding the implication that “any nucleic acid molecule” (the Action bridging pages 2 and 3) could be so used, Applicants first point out that only expressed sequences can be used in the identification of coding sequence, not just any nucleic acid. Applicants reiterate that the requirements of a specific utility, which is the proper standard for utility under 35 U.S.C. § 101, should not be confused with the requirement for a unique utility, which is clearly an improper standard (*Carl Zeiss Stiftung v. Renishaw PLC, supra*). The fact that a small number of other nucleotide sequences could be used to map the protein coding regions in this specific region of chromosome 2 does not mean that the use of Applicants’ sequence to map the protein coding regions of chromosome 2 is not a specific utility. Once again, the question of whether or not other nucleic acid sequences can be so used is completely irrelevant to the present utility inquiry. The only relevant question in regard to meeting the standards of 35 U.S.C. § 101 is whether every nucleic acid can be so used - and the clear answer to this question is once again an emphatic no. Applicants respectfully point out that in this case the Examiner is once again attempting to narrow the broad class of “any nucleic acid molecule” to include only those nucleic acid molecules that are expressed in order to support the allegation that the claimed nucleic acids lack a patentable utility, which Applicants point out once again is improper under the law as well as the policy of the USPTO. Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101.

Rather, as set forth by the Federal Circuit, “(t)he threshold of utility is not high: An invention is ‘useful’ under section 101 if it is capable of providing some identifiable benefit.” *Juicy Whip Inc. v. Orange Bang Inc.*, 51 USPQ2d 1700 (Fed. Cir. 1999) (citing *Brenner v. Manson*, 383 U.S. 519, 534 (1966)). Additionally, the Federal Circuit has stated that “(t)o violate § 101 the claimed device must be totally incapable of achieving a useful result.” *Brooktree Corp. v. Advanced Micro Devices, Inc.*, 977 F.2d 1555, 1571 (Fed. Cir. 1992), emphasis added. *Cross v. Iizuka* (224 USPQ 739 (Fed. Cir. 1985); “*Cross*”) states “any utility of the claimed compounds is sufficient to satisfy 35 U.S.C. § 101”. *Cross* at 748, emphasis added. Indeed, the Federal Circuit recently emphatically confirmed that “anything under the sun that is made by man” is patentable (*State Street Bank & Trust Co. v. Signature Financial Group Inc.*, 47 USPQ2d 1596, 1600 (Fed. Cir. 1998), citing the U.S. Supreme Court's decision in *Diamond vs. Chakrabarty*, 206 USPQ 193 (S.Ct. 1980)).

Finally, the requirements set forth in the Action for compliance with 35 U.S.C. § 101 do not comply with the requirements set forth by the Patent and Trademark Office (“the PTO”) itself for compliance with 35 U.S.C. § 101. While Applicants are well aware of the new Utility Guidelines set forth by the USPTO, Applicants respectfully point out that the current rules and regulations regarding the examination of patent applications is and always has been the patent laws as set forth in 35 U.S.C. and the patent rules as set forth in 37 C.F.R., not the Manual of Patent Examination Procedure or particular guidelines for patent examination set forth by the USPTO. Furthermore, it is the job of the judiciary, not the USPTO, to interpret these laws and rules. Applicants are unaware of any significant recent changes in either 35 U.S.C. § 101, or in the interpretation of 35 U.S.C. § 101 by the Supreme Court or the Federal Circuit that is in keeping with the new Utility Guidelines set forth by the USPTO. This is underscored by numerous patents that have been issued over the years that claim nucleic acid fragments that do not comply with the new Utility Guidelines. As examples of such issued U.S. Patents, the Examiner is invited to review U.S. Patent Nos. 5,817,479, 5,654,173, and 5,552,281 (each of which claims short polynucleotides; **Exhibits J-L**; copies of issued U.S. Patents not provided pursuant to requests from the USPTO), and recently issued U.S. Patent No. 6,340,583 (which includes no working examples; **Exhibit M**; copies of issued U.S. Patents not provided pursuant to requests from the USPTO), none of which contain examples of the “real-world” utilities that the Examiner seems to be requiring. As issued U.S. Patents are presumed to meet all of the requirements for patentability, including 35 U.S.C. §§ 101 and 112, first paragraph (see Section IV, below), Applicants submit that the present polynucleotides must also meet the requirements of 35 U.S.C. § 101. While Applicants understand that each application is examined on its own merits, Applicants are unaware of any changes to 35 U.S.C. § 101, or in the interpretation of 35 U.S.C. § 101 by the Supreme Court or the Federal Circuit, since the issuance of these patents that render the subject matter claimed in these patents, which is similar to the subject matter in question in the present application, as suddenly non-statutory or failing to meet the requirements of 35 U.S.C. § 101. Thus, holding Applicants to a different standard of utility would be arbitrary and capricious, and, like other clear violations of due process, cannot stand.

For each of the foregoing reasons, Applicants submit that as the presently claimed nucleic acid molecules have been shown to have a substantial, specific, credible and well-established utility, the rejection of claims 1-3 under 35 U.S.C. § 101 has been overcome, and request that the rejection be

withdrawn.

**IV. Rejection of Claims 1-3 Under 35 U.S.C. § 112, First Paragraph**

The Action next rejects claims 1-3 under 35 U.S.C. § 112, first paragraph, since allegedly one skilled in the art would not know how to use the invention, as the invention allegedly is not supported by a specific, substantial, and credible utility or a well-established utility. Applicants respectfully traverse.

Applicants submit that as claims 1-3 have been shown to have “a specific, substantial, and credible utility”, as detailed in section III above, the present rejection of claims 1-3 under 35 U.S.C. § 112, first paragraph, cannot stand.

Applicants therefore request that the rejection of claims 1-3 under 35 U.S.C. § 112, first paragraph, be withdrawn.

**V. Rejection of Claims 1-3 Under 35 U.S.C. § 112, First Paragraph**

The Action next rejects claims 1-3 under 35 U.S.C. § 112, first paragraph, for allegedly failing to comply with the enablement requirement. Applicants respectfully traverse.

The Action states that “(e)ven in the case that the claimed polynucleotides were shown to be supported by a specific and substantial utility, the Specification does not provide support for using the claimed polynucleotides in any methods of treatment or diagnosis or methods of screening for drugs” (Action at page 7). Applicants point out that the above comment is completely irrelevant to determining whether the claimed compositions meet the legal requirements for patentability under 35 U.S.C. § 112, first paragraph (*In re Brana, supra*). Furthermore, all of the Examiner’s arguments in support of this rejection center on the assertion that the presently claimed sequences do not have a patentable utility. Therefore, this rejection appears to merely be a reiteration of the rejection of claims 1-3 under 35 U.S.C. § 112, first paragraph, that is related to the utility rejection (see Section IV, above). As such, this rejection has been overcome, as discussed in detail in Sections III and IV, above.

Nevertheless, Applicants additionally submit that the Examiner has failed to present reasoning sufficient to establish a *prima facie* case supporting the present § 112 rejection, and accordingly the rejection is improper because: 1) the Examiner’s comments were not relevant to the established legal

standard of enablement; 2) the Examiner's failure to attribute adequate weight and attention to the detailed level of teaching clearly provided in the specification; and 3) the reasoning for the enablement rejection provided by the Examiner failed to adequately consider the high level of technical knowledge that can be attributed to those skilled in the art in the field of the present invention.

In attempting to establish a *prima facie* case to support the § 112 rejection of the composition claims, the Action questions whether the claimed compositions are sufficiently enabled to allow those skilled in the art to practice aspects of the invention involving standard molecular biological techniques. The § 112 rejection, as applied against the nucleic acid compositions, is completely misplaced. It has long been established that composition claims are enabled by defining any practical use of the claimed compound. *In re Nelson*, 126 USPQ 242 (CCPA 1960); *Cross v. Iizuka, supra*. "The enablement requirement is met if the description enables any mode of making and using the invention." *Johns Hopkins Univ. v. CellPro, Inc.*, 47 USPQ2d 1705, 1719 (Fed. Cir. 1998), citing *Engel Indus., Inc. v. Lockformer Co.*, 20 USPQ2d 1300, 1304 (Fed. Cir. 1991).

The Action seems to contend that the specification provides insufficient guidance regarding the biological function or activity of certain of the claimed compositions. However, such an enablement standard conflicts with established patent law. As discussed in Section III, above, in *In re Brana, supra*, the Federal Circuit admonished the USPTO for confusing "the requirements under the law for obtaining a patent with the requirements for obtaining government approval to market a particular drug for human consumption". *Brana* at 1442.

The Examiner states that the present invention could not be practiced without "undue experimentation" (Action at page 9). However, it is important to remember that, as discussed above in Section III, in assessing the question of whether undue experimentation would be required in order to practice the claimed invention, the key term is "undue", not "experimentation". *In re Angstadt and Griffin, supra*. In *Wands, supra*, the USPTO took the position that the applicant failed to demonstrate that the disclosed biological processes of immunization and antibody selection could reproducibly result in a useful biological product (antibodies from hybridomas) within the scope of the claims. In its decision overturning the USPTO's rejection, the Federal Circuit found that Wands' demonstration of success in four out of nine cell lines screened was sufficient to support a conclusion of enablement. The court emphasized that the need for some experimentation requiring, *e.g.*, production

of the biological material followed by routine screening, was not a basis for a finding of non-enablement, stating:

Disclosure in application for the immunoassay method patent does not fail to meet enablement requirement of 35 USC 112 by requiring 'undue experimentation,' even though production of monoclonal antibodies necessary to practice invention first requires production and screening of numerous antibody producing cells or 'hybridomas,' since practitioners of art are prepared to screen negative hybridomas in order to find those that produce desired antibodies, since in monoclonal antibody art one 'experiment' is not simply screening of one hybridoma but rather is entire attempt to make desired antibody, and since record indicates that amount of effort needed to obtain desired antibodies is not excessive, in view of Applicants' success in each attempt to produce antibody that satisfied all claim limitations.

*Wands* at 1400. Thus, the need for some experimentation does not render the claimed invention unpatentable under 35 U.S.C. § 112, first paragraph. Indeed, a considerable amount of experimentation may be permissible if such experimentation is routinely practiced in the art. *In re Angstadt and Griffin, supra; Amgen, Inc. v. Chugai Pharmaceutical Co., Ltd., supra.*

Applicants point out that numerous uses of the claimed sequences do not require knowledge of any functional aspects of the amino acid sequences. Significant commercial exploitation of nucleic acid sequences requires no more information than the nucleic acid sequence itself. Applications ranging from gene expression analysis or profiling (utilizing, for example, arrays of short, overlapping or non-overlapping, oligonucleotides and DNA chips, as described in Section III, above) to chromosomal mapping (utilizing, for example, short oligonucleotide probes or full length DNA sequences, as described in Section III, above) are practiced utilizing nucleic acid sequences and techniques that are well-known to those of skill in the art. The widespread commercial exploitation of nucleic acid sequence information points to the level of skill in the art, and the enablement provided by disclosures such as the present specification, which include specific nucleic acid sequences and guidance regarding the various uses of such sequences.

Even though the burden has been improperly shifted to Applicants, the following section is being provided to demonstrate that the specification is fully enabling in view of the detailed guidance and teaching provided in the specification within the context of the high level of technical knowledge present in the art regarding the use of nucleic acids such as those presently claimed.



The Action questions the teaching and guidance in the specification for certain aspects of the present invention. However, as discussed above, this requirement is completely misplaced. There is sufficient knowledge and technical skill in the art for a skilled artisan to be able to make and use the claimed DNA species in a number of different aspects of the invention entirely without further details in a patent specification. For example, it is not unreasonable to expect a Ph.D. level molecular biologist to be able to use the disclosed sequence to design oligonucleotide probes and primers and use them in, for example, PCR based screening and detection methods to obtain the described sequences and/or determine tissue expression patterns. Nevertheless, the present specification provides highly detailed descriptions of techniques that can be used to accomplish many different aspects of the claimed invention, including recombinant expression, site-specific mutagenesis, *in situ* hybridization, and large scale nucleic acid screening techniques, and properly incorporates by reference a montage of standard texts into the specification, such as Sambrook *et al.* (*Molecular Cloning, A Laboratory Manual*) and Ausubel *et al.* (*Current Protocols in Molecular Biology*) to provide even further guidance to the skilled artisan. Incorporation of material into the specification by reference is proper. *Ex parte Schwarze*, 151 USPQ 426 (PTO Bd. App. 1966). The § 112, first paragraph rejection is thus *prima facie* improper:

As a matter of patent office practice, then, a specification disclosure which contains a teaching of the manner and process of making and using the invention in terms which correspond in scope to those used in describing and defining the subject matter sought to be patented must be taken as in compliance with the enabling requirement of the first paragraph of § 112 unless there is reason to doubt the objective truth of the statements contained therein which must be relied on for enabling support.

*In re Marzocchi, supra*, emphasis as in original. In any event, an alleged lack of express teaching is insufficient to support a first paragraph rejection where one of skill in the art would know how to perform techniques required to perform at least one aspect of the invention. As a matter of law, it is well settled that a patent need not disclose what is well known in the art. *In re Wands, supra*. In fact, it is preferable that what is well known in the art be omitted from the disclosure. *Hybritech, Inc. v. Monoclonal Antibodies, Inc.*, 231 USPQ 81 (Fed. Cir. 1986). As standard molecular biological techniques are routine in the art, such protocols do not need to be described in detail in the specification.

Furthermore, a specification “need describe the invention only in such detail as to enable a person skilled in the most relevant art to make and use it.” *In re Naquin*, 158 USPQ 317, 319

(CCPA 1968); emphasis added. The present claims are thus enabled as they are supported by a specification that provides sufficient description to enable the skilled person to make and use the invention as claimed.

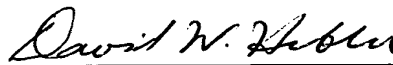
Therefore, as all aspects of the enablement rejection have been overcome, Applicants respectfully request that the rejection of claims 1-3 under 35 U.S.C. § 112, first paragraph be withdrawn.

## **VI. Conclusion**

The present document is a full and complete response to the Action. In conclusion, Applicants submit that, in light of the foregoing remarks, the present case is in condition for allowance, and such favorable action is respectfully requested. Should Examiner Schnizer have any questions or comments, or believe that certain amendments of the claims might serve to improve their clarity, a telephone call to the undersigned Applicants' representative is earnestly solicited.

Respectfully submitted,

July 29, 2004  
Date



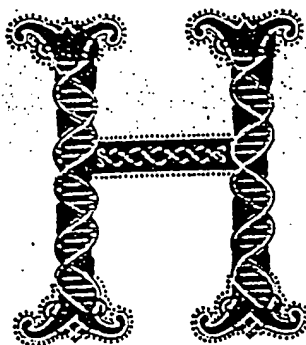
David W. Hibler  
Agent for Applicants

Reg. No. 41,071

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8800 Technology Forest Place  
The Woodlands, TX 77381  
(281) 863-3399

**Customer # 24231**

# THE HUMAN GENOME



umanity has been given a great gift. With the completion of the human genome sequence, we have received a powerful tool for unlocking the secrets of our genetic heritage and for finding our place among the other participants in the adventure of life.

This week's issue of *Science* contains the report of the sequencing of the human genome from a group of authors led by Craig Venter of Celera Genomics. The report of the sequencing of the human genome from the publicly funded consortium of laboratories led by Francis Collins appears in this week's *Nature*. This stunning achievement has been portrayed—

often unfairly—as a competition between two ventures, one public and one private. That characterization detracts from the awesome accomplishment jointly unveiled this week. In truth, each project contributed to the other. The inspired vision that launched the publicly funded project roughly 10 years ago reflected, and now rewards, the confidence of those who believe that the pursuit of large-scale fundamental problems in the life sciences is in the national interest. The technical innovation and drive of Craig Venter and his colleagues made it possible to celebrate this accomplishment far sooner than was believed possible. Thus, we can salute what has become, in the end, not a contest but a marriage (perhaps encouraged by shotgun) between public funding and private entrepreneurship.

There are excellent scientific reasons for applauding an outcome that has given us two winners. Two sequences are better than one; the opportunity for comparison and convergence is invaluable. Indeed, a real-world proof of the importance of access to both sets of data can be found in the pages of this issue of *Science*, in the comparative analysis by Olivier *et al.* (p. 1298).

Although we have made the point before, it is worth repeating that the sequencing of the human genome represents, not an ending, but the beginning of a new approach to biology. As Galas says in his Viewpoint (p. 1257), the knowledge that all of the genetic components of any process can be identified will give extraordinary new power to scientists. Because of this breakthrough, research can evolve from analyzing the effects of individual genes to a more integrated view that examines whole ensembles of genes as they interact to form a living human being. Several articles in this issue highlight how this approach is already beginning to revolutionize the way we look at human disease.

This has been a massive project, on a scale unparalleled in the history of biology, but of course it has built on the scientific insights of centuries of investigators. By coincidence, this landmark announcement falls during the week of the anniversary of the birth of Charles Darwin. Darwin's message that the survival of a species can depend on its ability to evolve in the face of change is peculiarly pertinent to discussions that have gone on in the past year over access to the Celera data. (Full information regarding the agreements that were reached to make the data available can be found at [www.sciencemag.org/feature/data/announcement/gsp.shl](http://www.sciencemag.org/feature/data/announcement/gsp.shl).) We are willing to be flexible in allowing data repositories other than the traditional GenBank, while insisting on access to all the data needed to verify conclusions. In this domain, change is everywhere: Commercial researchers are producing more and more potentially valuable sequences, yet (at least in the United States) laws governing databases provide scant protection against piracy. Had the Celera data been kept secret, it would have been a serious loss to the scientific community. We hope that our adaptability in the face of change will enable other proprietary data to be published after peer review, in a way that satisfies our continuing commitment to full access.

It should be no surprise that an achievement so stunning, and so carefully watched, has created new challenges for the scientific venture. *Science* is proud to have played a role in bringing this discovery onto the public stage. It is literally true that this is a historic moment for the scientific endeavor. The human genome has been called the Book of Life. Rather, it is a library, in which, with rules that encourage exploration and reward creativity, we can find many of the books that will help define us and our place in the great tapestry of life.

Barbara R. Jasny and Donald Kennedy

**A historic  
moment for  
the scientific  
endeavor.**

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Query: 2033 taacgggcagcagtgaaagcctgtggaaaggggttacaacaagag 2077  
|||||  
Sbjct: 27435 taacgggcagcagtgaaagcctgtggaaaggggttacaacaagag 27391

>AC016679.9.1.89212  
Length = 89212

Score = 387 bits (195), Expect = e-104  
Identities = 195/195 (100%)  
Strand = Plus / Plus

Query: 4034 aggggtggagtctgtggttggtgagaagggctatacagagataatgaaatcaaattggtttcc 4093  
|||||  
Sbjct: 12254 aggggtggagtctgtggttggtgagaagggctatacagagataatgaaatcaaattggtttcc 12313

Query: 4094 tggattactgcatgaaagtaccaggctcagaggataaaaaagctgatgtgaaaaaccttt 4153  
|||||  
Sbjct: 12314 tggattactgcatgaaagtaccaggctcagaggataaaaaagctgatgtgaaaaaccttt 12373

Query: 4154 ctgggaaaaacagacctgtgaattcaaaaatacatgatatttttaaaggatgggtctcttc 4213  
|||||  
Sbjct: 12374 ctgggaaaaacagacctgtgaattcaaaaatacatgatatttttaaaggatgggtctcttc 12433

Query: 4214 aaccacttgatccag 4228  
|||||  
Sbjct: 12434 aaccacttgatccag 12448

Score = 355 bits (179), Expect = 2e-94  
Identities = 179/179 (100%)  
Strand = Plus / Plus

Query: 3679 ccaggagactgccatttaacagaatgggtcagagtgaggagcacatgtgaattaacctgcatt 3738  
|||||  
Sbjct: 5665 ccaggagactgccatttaacagaatgggtcagagtgaggagcacatgtgaattaacctgcatt 5724

Query: 3739 gatggaagaagctttgagactgtgggccgccagtcctagatcaaggacttttataattcag 3798  
|||||  
Sbjct: 5725 gatggaagaagctttgagactgtgggccgccagtcctagatcaaggacttttataattcag 5784

Query: 3799 tcttttgagaaccaagacagctgcccccaacagggttctagaaacacgcccttgtagagg 3857  
|||||  
Sbjct: 5785 tcttttgagaaccaagacagctgcccccaacagggttctagaaacacgcccttgtagagg 5843

Score = 323 bits (163), Expect = 5e-85  
Identities = 163/163 (100%)  
Strand = Plus / Plus

Query: 3521 aggggtggagactgtggggaaggagttcagatccgcagcctttcctgcatggtccacagt 3580  
|||||  
Sbjct: 4372 aggggtggagactgtggggaaggagttcagatccgcagcctttcctgcatggtccacagt 4431

Query: 3581 gttcaatatctcatgcagctggacgtgtcgaggatgcactgtgtggagaaatgccctttc 3640  
|||||  
Sbjct: 4432 gttcaatatctcatgcagctggacgtgtcgaggatgcactgtgtggagaaatgccctttc 4491

Query: 3641 aggacagcatcctgaagcagctgtgttctgtgccttgcccagg 3683  
|||||  
Sbjct: 4492 aggacagcatcctgaagcagctgtgttctgtgccttgcccagg 4534

Score = 202 bits (102), Expect = 1e-48  
Identities = 102/102 (100%)  
Strand = Plus / Plus

Query: 3852 tacaggaggcaaatgttatcactacacatggaaagcaagtctttggaacaataacgaacg 3911  
|||||  
Sbjct: 5933 tacaggaggcaaatgttatcactacacatggaaagcaagtctttggaacaataacgaacg 5992

Query: 3912 aactgtatggtgccagcggttcagatggcggttaatgtcacagg 3953  
|||||  
Sbjct: 5993 aactgtatggtgccagcggttcagatggcggttaatgtcacagg 6034

Score = 180 bits (91), Expect = 5e-42  
Identities = 91/91 (100%)  
Strand = Plus / Plus

Query: 4226 cagatggccgagtaaaaatttgggtttatggcgtttcaggtggcgcttttctcatcatga 4285  
|||||  
Sbjct: 16644 cagatggccgagtaaaaatttgggtttatggcgtttcaggtggcgcttttctcatcatga 16703

Query: 4286 ttttcctaataatttacttcctaccttggttg 4316  
|||||  
Sbjct: 16704 ttttcctaataatttacttcctaccttggttg 16734

Score = 172 bits (87), Expect = 1e-39  
Identities = 87/87 (100%)  
Strand = Plus / Plus

Query: 3950 caggaggctgctcccctcaggcccgctcctgctgccattcggcagtgccattccagcctgca 4009  
|||||  
Sbjct: 8534 caggaggctgctcccctcaggcccgctcctgctgccattcggcagtgccattccagcctgca 8593

Query: 4010 gaaaacctttctcctactgtacacagg 4036  
|||||  
Sbjct: 8594 gaaaacctttctcctactgtacacagg 8620

Score = 165 bits (83), Expect = 3e-37  
Identities = 83/83 (100%)  
Strand = Plus / Plus

Query: 4316 gcaagaagccaaaaccacatcaaagcacacctccccaacagaagcctctgaccttagcct 4375  
|||||  
Sbjct: 25396 gcaagaagccaaaaccacatcaaagcacacctccccaacagaagcctctgaccttagcct 25455

Query: 4376 acgatggagacttagacatgtaa 4398  
|||||  
Sbjct: 25456 acgatggagacttagacatgtaa 25478

>AC017082.4.1.183783  
Length = 183783

Score = 305 bits (154), Expect = 1e-79  
Identities = 154/154 (100%)  
Strand = Plus / Minus

Query: 2847 cagatgtgtgaatactgcggtggtgaaggtggagcagtggtatagcaacctgtgcaacca 2906  
|||||  
Sbjct: 80725 cagatgtgtgaatactgcggtggtgaaggtggagcagtggtatagcaacctgtgcaacca 80666

Query: 2907 ggatgaaattccccagaaacccagtcctgttctcttatgtgtcccaatgagtgtgtcat 2966  
|||||  
Sbjct: 80665 ggatgaaattccccagaaacccagtcctgttctcttatgtgtcccaatgagtgtgtcat 80606

Query: 2967 gtctgagtggggactttggagcaaagtcccacag 3000  
|||||  
Sbjct: 80605 gtctgagtggggactttggagcaaagtcccacag 80572

Score = 295 bits (149), Expect = 1e-76  
Identities = 149/149 (100%)  
Strand = Plus / Minus

Query: 3375 aggtcgaatgagccggactcgatttatcattatgccaaaccaaggagaaggacggccatg 3434  
|||||  
Sbjct: 10642 aggtcgaatgagccggactcgatttatcattatgccaaaccaaggagaaggacggccatg 10583

Query: 3435 cccacagagcttaccaggagaaaacctgcccagtgacccctgctacagctgggtcct 3494  
|||||  
Sbjct: 10582 cccacagagcttaccaggagaaaacctgcccagtgacccctgctacagctgggtcct 10523

Query: 3495 tggcaactggtctgcatgtaaattggagg 3523  
|||||  
Sbjct: 10522 tggcaactggtctgcatgtaaattggagg 10494

Score = 285 bits (144), Expect = 1e-73  
Identities = 144/144 (100%)  
Strand = Plus / Minus

Query: 2999 agtcatgcatccccacacaatgcagagaagaactcgccacctgctaagaccatcactga 3058  
|||||  
Sbjct: 36955 agtcatgcatccccacacaatgcagagaagaactcgccacctgctaagaccatcactga 36896

Query: 3059 actcaaggacttgtgctgaagactcacaggtgcagccttgccctcctgaatgaaaattgct 3118  
|||||  
Sbjct: 36895 actcaaggacttgtgctgaagactcacaggtgcagccttgccctcctgaatgaaaattgct 36836

Query: 3119 tccagttccagtacaatctaacag 3142  
|||||  
Sbjct: 36835 tccagttccagtacaatctaacag 36812

Score = 281 bits (142), Expect = 2e-72  
Identities = 145/146 (99%)  
Strand = Plus / Minus

Query: 2713 caggtacatgaggcagtcctcatgttacagtgagtgcaatcagtattcctgggttgtagaa 2772  
|||||  
Sbjct: 89910 caggtacatgaggcagtcctcatgttacagtgagtgcaatcagtattcctgggttgtagaa 89851

Query: 2773 cactgggtcttcatgcaaaatcaacaatgagctgaggtccctgcgctgtggaggaggaaca 2832  
|||||  
Sbjct: 89850 cactgggtcttcatgcaaaatcaacaatgagctgaggtccctgcgctgtggaggaggaaca 89791

Query: 2833 caatctaggaaaatcagatgtgtgaa 2858  
|||||  
Sbjct: 89790 caatctaggaaaatcaggtgtgtgaa 89765

Score = 246 bits (124), Expect = 1e-61  
Identities = 124/124 (100%)  
Strand = Plus / Minus

Query: 3255 gcagcataatttgagagaagccccagagaatgagcattccctgcttggtggaatgcgtggt 3314  
|||||  
Sbjct: 32523 gcagcataatttgagagaagccccagagaatgagcattccctgcttggtggaatgcgtggt 32464

Query: 3315 caactgtcagctctcaggggtggacggccttggacagagtgttcacagacctgtggccatgg 3374  
|||||  
Sbjct: 32463 caactgtcagctctcaggggtggacggccttggacagagtgttcacagacctgtggccatgg 32404

Query: 3375 aggt 3378  
||||  
Sbjct: 32403 aggt 32400

Score = 234 bits (118), Expect = 4e-58  
Identities = 118/118 (100%)  
Strand = Plus / Minus

Query: 3141 agagtggagcacatgccagctgagtgaaaacgcaccctgtggtcaaggcgtcaggacccg 3200  
|||||  
Sbjct: 34738 agagtggagcacatgccagctgagtgaaaacgcaccctgtggtcaaggcgtcaggacccg 34679

Query: 3201 cctgctaagctgtgtgtgcagtgatggcaagccagtcagcatggaccaatgtgagcag 3258  
|||||  
Sbjct: 34678 cctgctaagctgtgtgtgcagtgatggcaagccagtcagcatggaccaatgtgagcag 34621

Query= SEQ ID NO:3  
(4773 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AC011231.7.1.119205	<u>1612</u>	0.0
AC019067.9.1.169928	<u>535</u>	e-149
AC012000.3.1.194472	<u>470</u>	e-129
AC016679.9.1.89212	<u>387</u>	e-104
AC017082.4.1.183783	<u>305</u>	1e-79
AC010873.12.1.180602	<u>184</u>	3e-43

>AC011231.7.1.119205  
Length = 119205

Score = 1612 bits (813), Expect = 0.0  
Identities = 813/813 (100%)  
Strand = Plus / Minus

Query: 90 aggtccgtggggaaggtgtacaggagactgtggtcccggaggagtccagagtcgggcagt 149  
|||||  
Sbjct: 52727 aggtccgtggggaaggtgtacaggagactgtggtcccggaggagtccagagtcgggcagt 52668

Query: 150 gtggtgttttcatgttgacgggtggacaagtcacctgtctaactgtggtgagagcaacag 209  
|||||  
Sbjct: 52667 gtggtgttttcatgttgacgggtggacaagtcacctgtctaactgtggtgagagcaacag 52608

Query: 210 gcctccaaaggaaagaagttgtttccgagtttgtgactggcacagtgcacctctttcagtg 269  
|||||  
Sbjct: 52607 gcctccaaaggaaagaagttgtttccgagtttgtgactggcacagtgcacctctttcagtg 52548

Query: 270 ggagggtttctgactggcaccactgtgtgcttggttccttacgctcgcggtgaagtcaagcc 329  
|||||  
Sbjct: 52547 ggagggtttctgactggcaccactgtgtgcttggttccttacgctcgcggtgaagtcaagcc 52488

Query: 330 tcggactgcagagtgtgtgacggctcagcatggactgcagcaccggatggtgcgctgcat 389  
|||||  
Sbjct: 52487 tcggactgcagagtgtgtgacggctcagcatggactgcagcaccggatggtgcgctgcat 52428

Query: 390 tcagaagctgaaccgaactgtggttgcaaataaaatgcaaacactttgcccttcagcc 449  
|||||  
Sbjct: 52427 tcagaagctgaaccgaactgtggttgcaaataaaatgcaaacactttgcccttcagcc 52368

Query: 450 tcctacagaacaggcttgccctattccttgccccgggattgtgtagtatctgagttcctt 509  
|||||  
Sbjct: 52367 tcctacagaacaggcttgccctattccttgccccgggattgtgtagtatctgagttcctt 52308



Query: 510 accatgggtccaactgtagcaagggatgtgggaagaaattgcagcatagaactcgcgcggt 569  
|||||  
Sbjct: 52307 accatgggtccaactgtagcaagggatgtgggaagaaattgcagcatagaactcgcgcggt 52248

Query: 570 catagctccccctctctttgggtggtttgcaatgtccaaatctgactgagtcaagagcctg 629  
|||||  
Sbjct: 52247 catagctccccctctctttgggtggtttgcaatgtccaaatctgactgagtcaagagcctg 52188

Query: 630 tgatgctcccatttctctgtcctcttggggaagaggaatatacatcttagccttaaggttgg 689  
|||||  
Sbjct: 52187 tgatgctcccatttctctgtcctcttggggaagaggaatatacatcttagccttaaggttgg 52128

Query: 690 accatggagtaaattgcagactgcctcatcttaaagaaattaatccaagcggaagaactgt 749  
|||||  
Sbjct: 52127 accatggagtaaattgcagactgcctcatcttaaagaaattaatccaagcggaagaactgt 52068

Query: 750 tctggattttaactctgattcaaatgagcgagtcacctttaaacatcaaagttacaaagc 809  
|||||  
Sbjct: 52067 tctggattttaactctgattcaaatgagcgagtcacctttaaacatcaaagttacaaagc 52008

Query: 810 acatcatcattcgaagtcttgggcaatagagataggttatcaaaccggcaggtttcgtg 869  
|||||  
Sbjct: 52007 acatcatcattcgaagtcttgggcaatagagataggttatcaaaccggcaggtttcgtg 51948

Query: 870 tacaagaagtgatggacaaaatgctatgttaag 902  
|||||  
Sbjct: 51947 tacaagaagtgatggacaaaatgctatgttaag 51915

Score = 507 bits (256), Expect = e-140  
Identities = 256/256 (100%)  
Strand = Plus / Minus

Query: 901 agcctttgccttcaagattccttcccattgactgttcagtcctgcatcatgcccaaagac 960  
|||||  
Sbjct: 14274 agcctttgccttcaagattccttcccattgactgttcagtcctgcatcatgcccaaagac 14215

Query: 961 tgtgaaacctcccagtggtcctcctggagccccctgctccaagacatgccgttcagggagt 1020  
|||||  
Sbjct: 14214 tgtgaaacctcccagtggtcctcctggagccccctgctccaagacatgccgttcagggagt 14155

Query: 1021 ctcttgccaggatttaggagcaggagccggaacgtgaagcacatggctattggaggtgga 1080  
|||||  
Sbjct: 14154 ctcttgccaggatttaggagcaggagccggaacgtgaagcacatggctattggaggtgga 14095

Query: 1081 aaggagtgtcctgaacttcttgagaaaggagcctgcattgttgaaggagaacttctgcag 1140  
|||||  
Sbjct: 14094 aaggagtgtcctgaacttcttgagaaaggagcctgcattgttgaaggagaacttctgcag 14035

Query: 1141 caatgtcccaggtatt 1156  
|||||  
Sbjct: 14034 caatgtcccaggtatt 14019

>AC019067.9.1.169928  
Length = 169928

Score = 535 bits (270), Expect = e-149  
Identities = 270/270 (100%)  
Strand = Plus / Minus

Query: 2644 acagggaaaagcagaaagaaggagaaatgccaggattctgacctttaccctctagtggag 2703  
|||||  
Sbjct: 59740 acagggaaaagcagaaagaaggagaaatgccaggattctgacctttaccctctagtggag 59681

Query: 2704 acagaactatgtccttgtgatgaatttatatcccaaccttatggaaactggtcagattgc 2763  
|||||  
Sbjct: 59680 acagaactatgtccttgtgatgaatttatatcccaaccttatggaaactggtcagattgc 59621

Query: 2764 attcttccagaaggcagaagggagcctcaccgaggactgcgggtacaagcagacagcaaa 2823  
|||||  
Sbjct: 59620 attcttccagaaggcagaagggagcctcaccgaggactgcgggtacaagcagacagcaaa 59561

Query: 2824 gaatgtggagaaggcctgcgctttcgagcagtagcctgttctgataaaaatggaagacct 2883  
|||||  
Sbjct: 59560 gaatgtggagaaggcctgcgctttcgagcagtagcctgttctgataaaaatggaagacct 59501

Query: 2884 gttgacccctccttctgcagcagctctggt 2913  
|||||  
Sbjct: 59500 gttgacccctccttctgcagcagctctggt 59471

Score = 392 bits (198), Expect = e-106  
Identities = 198/198 (100%)  
Strand = Plus / Minus

Query: 2451 agctgtctcatgcatctctgatgacaaccggtcagcagaaatgatggaatgcctcaagca 2510  
|||||  
Sbjct: 65734 agctgtctcatgcatctctgatgacaaccggtcagcagaaatgatggaatgcctcaagca 65675

Query: 2511 gacaaacggcatgcctctccttgtgcaagaatgcacagtcccatgtcgagaagactgcac 2570  
|||||  
Sbjct: 65674 gacaaacggcatgcctctccttgtgcaagaatgcacagtcccatgtcgagaagactgcac 65615

Query: 2571 cttcactgcttgggtccaagtttacgccctgctccacgaactgtgaagccacaaaaagtag 2630  
|||||  
Sbjct: 65614 cttcactgcttgggtccaagtttacgccctgctccacgaactgtgaagccacaaaaagtag 65555

Query: 2631 gcggcgacagctcacagg 2648  
|||||  
Sbjct: 65554 gcggcgacagctcacagg 65537

Score = 363 bits (183), Expect = 7e-97  
Identities = 183/183 (100%)  
Strand = Plus / Minus

Query: 2911 ggttacattcaagaaaaatgtgtcattccctgccatttgattgcaagttaagcgattgg 2970  
|||||  
Sbjct: 20501 ggttacattcaagaaaaatgtgtcattccctgccatttgattgcaagttaagcgattgg 20442

Query: 2971 tctagttgggggtcttgcagttcatcttgtggaattggagtgagaattcgatccaaatgg 3030  
|||||  
Sbjct: 20441 tctagttgggggtcttgcagttcatcttgtggaattggagtgagaattcgatccaaatgg 20382

Query: 3031 ctaaaagaaaaaccttacaatggaggacgaccatgtcccaaactggatctcaagaatcag 3090  
|||||  
Sbjct: 20381 ctaaaagaaaaaccttacaatggaggacgaccatgtcccaaactggatctcaagaatcag 20322

Query: 3091 gta 3093  
|||  
Sbjct: 20321 gta 20319

>AC012000.3.1.194472  
Length = 194472

Score = 470 bits (237), Expect = e-129  
Identities = 237/237 (100%)  
Strand = Plus / Minus

Query: 1866 aggtggaaagccatgtccccctagtcaggctctccaagagcatcgtttgtgtaatgacca 1925  
|||||  
Sbjct: 70520 aggtggaaagccatgtccccctagtcaggctctccaagagcatcgtttgtgtaatgacca 70461

Query: 1926 ttctctgtatgcagcttcactgggagacatcgcccttggggcccttggttctgaggacacatt 1985  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 70460 ttctctgtatgcagcttcactgggagacatcgcccttggggcccttggttctgaggacacatt 70401

Query: 1986 ggtaactgcccttaatgcaaccattggctggaatggagaagccacgtgtggtgtaggcat 2045  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 70400 ggtaactgcccttaatgcaaccattggctggaatggagaagccacgtgtggtgtaggcat 70341

Query: 2046 tcagactcggagagtcttctgtgtcaagagtcacgtgggacaagtaatgacccaaaag 2102  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 70340 tcagactcggagagtcttctgtgtcaagagtcacgtgggacaagtaatgacccaaaag 70284

Score = 398 bits (201), Expect = e-107  
Identities = 201/201 (100%)  
Strand = Plus / Minus

Query: 1476 aggatttagaacgaggcagcgccatgtcctcatggaatctacagggcctgcagggcattg 1535  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 132678 aggatttagaacgaggcagcgccatgtcctcatggaatctacagggcctgcagggcattg 132619

Query: 1536 ccctcatttggtggagctctgttccttgtaggatccaatgtgctaccgatggctggcatc 1595  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 132618 ccctcatttggtggagctctgttccttgtaggatccaatgtgctaccgatggctggcatc 132559

Query: 1596 agaagggatctgtttccctgatcatggaaaatgtggcctgggacatcgtattctgaaggc 1655  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 132558 agaagggatctgtttccctgatcatggaaaatgtggcctgggacatcgtattctgaaggc 132499

Query: 1656 cgtctgccagaatgaccgcgg 1676  
||||||||||||||||  
Sbjct: 132498 cgtctgccagaatgaccgcgg 132478

Score = 389 bits (196), Expect = e-104  
Identities = 196/196 (100%)  
Strand = Plus / Minus

Query: 1675 ggagaagatgtatcagggagtctttgccagttccccctcctcctgagaggaagtcttgt 1734  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 72374 ggagaagatgtatcagggagtctttgccagttccccctcctcctgagaggaagtcttgt 72315

Query: 1735 gaaattccctgccgaatggactgtgtgctgagcgagtggacggagtggcatcctgttcc 1794  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 72314 gaaattccctgccgaatggactgtgtgctgagcgagtggacggagtggcatcctgttcc 72255

Query: 1795 cagtcctgtttcaaataaaaaactcagatgggaaacagaccaggtcaagaactatcctggca 1854  
|||||  
Sbjct: 72254 cagtcctgtttcaaataaaaaactcagatgggaaacagaccaggtcaagaactatcctggca 72195

Query: 1855 ctggctggggaaggtg 1870  
|||||  
Sbjct: 72194 ctggctggggaaggtg 72179

Score = 343 bits (173), Expect = 6e-91  
Identities = 173/173 (100%)  
Strand = Plus / Minus

Query: 1149 caggatttcctggagaacttctgaatggaaagaatgccaggtctctctcctcctcgagca 1208  
|||||  
Sbjct: 188296 caggatttcctggagaacttctgaatggaaagaatgccaggtctctctcctcctcgagca 188237

Query: 1209 gcaggatccccactggcatgtgacgggacccgtgtgtggcggtgggatccagacccggga 1268  
|||||  
Sbjct: 188236 gcaggatccccactggcatgtgacgggacccgtgtgtggcggtgggatccagacccggga 188177

Query: 1269 ggtgtactgtgcccagagcgtaccagcagctgccgcactgagggccaaggaag 1321  
|||||  
Sbjct: 188176 ggtgtactgtgcccagagcgtaccagcagctgccgcactgagggccaaggaag 188124

Score = 307 bits (155), Expect = 3e-80  
Identities = 158/159 (99%)  
Strand = Plus / Minus

Query: 1320 agtctctagacctgtggaaaaggcattatgtgtgggacccgccccgttgccctctcagct 1379  
|||||  
Sbjct: 143206 agtctctagacctgtggaaaaggcattatgtgtgggacccgccccgttgccctctcagct 143147

Query: 1380 ctgcaatatcccttgctctacggactgcatagtatcttcctggtcagcctggggcctgtg 1439  
|||||  
Sbjct: 143146 ctgcaatatcccttgctctacggactgcatagtatcttcctggtcagcctggggcctgtg 143087

Query: 1440 catccatgaaaactgtcatgaacctcaggggaaaaaagg 1478  
|||||  
Sbjct: 143086 catccatgaaaactgtcatgatcctcaggggaaaaaagg 143048

Score = 266 bits (134), Expect = 1e-67  
Identities = 134/134 (100%)  
Strand = Plus / Minus

Query: 2216 caggaaatgccacagtaaaacagtctcgatacagaatcatcatccaagaagcagccaatg 2275  
|||||  
Sbjct: 30887 caggaaatgccacagtaaaacagtctcgatacagaatcatcatccaagaagcagccaatg 30828

Query: 2276 gagggccaggaatgccagataccttatatgaggagagagagtgtgaagatgtttccttgt 2335  
|||||  
Sbjct: 30827 gagggccaggaatgccagataccttatatgaggagagagagtgtgaagatgtttccttgt 30768

Query: 2336 gtcctgtatatcgg 2349  
|||||  
Sbjct: 30767 gtcctgtatatcgg 30754

Score = 236 bits (119), Expect = 1e-58  
Identities = 119/119 (100%)  
Strand = Plus / Minus

Query: 2101 agatgtccagattctactcgacctgaaactgtgcgccccctgttttctcccatgcaaaaaa 2160  
|||||  
Sbjct: 60962 agatgtccagattctactcgacctgaaactgtgcgccccctgttttctcccatgcaaaaaa 60903

Query: 2161 gactgtattgtgactgctttcagtgagtggacaccctgccaaggatgtgccaagcagg 2219  
|||||  
Sbjct: 60902 gactgtattgtgactgctttcagtgagtggacaccctgccaaggatgtgccaagcagg 60844

Score = 208 bits (105), Expect = 2e-50  
Identities = 105/105 (100%)  
Strand = Plus / Minus

Query: 2348 ggtggaagccacagaaatggagcccttgcatcttagtgccagagtctgtctggcagggaa 2407  
|||||  
Sbjct: 27495 ggtggaagccacagaaatggagcccttgcatcttagtgccagagtctgtctggcagggaa 27436

Query: 2408 taacgggcagcagtgaagcctgtggaaaggggttacaacaagag 2452  
|||||  
Sbjct: 27435 taacgggcagcagtgaagcctgtggaaaggggttacaacaagag 27391

>AC016679.9.1.89212

Length = 89212

Score = 387 bits (195), Expect = e-104

Identities = 195/195 (100%)

Strand = Plus / Plus

Query: 4409 aggggtggagtcctgtggttgtgagaagggctatacagagataatgaaatcaaattggtttcc 4468  
|||||

Sbjct: 12254 aggggtggagtcctgtggttgtgagaagggctatacagagataatgaaatcaaattggtttcc 12313

Query: 4469 tggattactgcatgaaagtaccaggctcagaggataaaaaagctgatgtgaaaaaccttt 4528  
|||||

Sbjct: 12314 tggattactgcatgaaagtaccaggctcagaggataaaaaagctgatgtgaaaaaccttt 12373

Query: 4529 ctgggaaaaacagacctgtgaattcaaaaatacatgatatttttaaggatgggtctcttc 4588  
|||||

Sbjct: 12374 ctgggaaaaacagacctgtgaattcaaaaatacatgatatttttaaggatgggtctcttc 12433

Query: 4589 aaccacttgatccag 4603  
|||||

Sbjct: 12434 aaccacttgatccag 12448

Score = 355 bits (179), Expect = 2e-94

Identities = 179/179 (100%)

Strand = Plus / Plus

Query: 4054 ccaggagactgccatttaacagaatgggtcagagtggagcacatgtgaattaacctgcatt 4113  
|||||

Sbjct: 5665 ccaggagactgccatttaacagaatgggtcagagtggagcacatgtgaattaacctgcatt 5724

Query: 4114 gatggaagaagctttgagactgtgggccgccagtctagatcaaggacttttataattcag 4173  
|||||

Sbjct: 5725 gatggaagaagctttgagactgtgggccgccagtctagatcaaggacttttataattcag 5784

Query: 4174 tcttttgagaaccaagacagctgcccccaacagggttctagaaacacgcccttgtagagg 4232  
|||||

Sbjct: 5785 tcttttgagaaccaagacagctgcccccaacagggttctagaaacacgcccttgtagagg 5843

Score = 323 bits (163), Expect = 6e-85  
Identities = 163/163 (100%)  
Strand = Plus / Plus

Query: 3896 aggggtggagactgtggggaaggagttcagatccgcagcctttcctgcatgggtccacagtg 3955  
|||||  
Sbjct: 4372 aggggtggagactgtggggaaggagttcagatccgcagcctttcctgcatgggtccacagtg 4431

Query: 3956 gttcaatatctcatgcagctggacgtgtcgaggatgcactgtgtggagaaatgccctttc 4015  
|||||  
Sbjct: 4432 gttcaatatctcatgcagctggacgtgtcgaggatgcactgtgtggagaaatgccctttc 4491

Query: 4016 aggacagcatcctgaagcagctgtgttctgtgccttgcccagg 4058  
|||||  
Sbjct: 4492 aggacagcatcctgaagcagctgtgttctgtgccttgcccagg 4534

Score = 202 bits (102), Expect = 1e-48  
Identities = 102/102 (100%)  
Strand = Plus / Plus

Query: 4227 tacaggaggcaaagtgttatcactacacatggaaagcaagtctttggaacaataacgaacg 4286  
|||||  
Sbjct: 5933 tacaggaggcaaagtgttatcactacacatggaaagcaagtctttggaacaataacgaacg 5992

Query: 4287 aactgtatggtgccagcggttcagatggcggttaatgtcacagg 4328  
|||||  
Sbjct: 5993 aactgtatggtgccagcggttcagatggcggttaatgtcacagg 6034

Score = 180 bits (91), Expect = 5e-42  
Identities = 91/91 (100%)  
Strand = Plus / Plus

Query: 4601 cagatggccgagtaaaaatttgggtttatggcgtttcaggtggcgcttttctcatcatga 4660  
|||||  
Sbjct: 16644 cagatggccgagtaaaaatttgggtttatggcgtttcaggtggcgcttttctcatcatga 16703

Query: 4661 ttttctaatatttacttcctaccttggttg 4691  
|||||  
Sbjct: 16704 ttttctaatatttacttcctaccttggttg 16734



Score = 172 bits (87), Expect = 1e-39  
Identities = 87/87 (100%)  
Strand = Plus / Plus

Query: 4325 caggaggctgctccccctcaggcccgctcctgctgccattcggcagtgccattccagcctgca 4384  
|||||  
Sbjct: 8534 caggaggctgctccccctcaggcccgctcctgctgccattcggcagtgccattccagcctgca 8593

Query: 4385 gaaaacctttctcctactgtacacagg 4411  
|||||  
Sbjct: 8594 gaaaacctttctcctactgtacacagg 8620

Score = 165 bits (83), Expect = 3e-37  
Identities = 83/83 (100%)  
Strand = Plus / Plus

Query: 4691 gcaagaagccaaaaccacatcaaagcacacctccccaacagaagcctctgaccttagcct 4750  
|||||  
Sbjct: 25396 gcaagaagccaaaaccacatcaaagcacacctccccaacagaagcctctgaccttagcct 25455

Query: 4751 acgatggagacttagacatgtaa 4773  
|||||  
Sbjct: 25456 acgatggagacttagacatgtaa 25478

>AC017082.4.1.183783  
Length = 183783

Score = 305 bits (154), Expect = 1e-79  
Identities = 154/154 (100%)  
Strand = Plus / Minus

Query: 3222 cagatgtgtgaatactgcggatggtgaaggtggagcagtgatagcaacctgtgcaacca 3281  
|||||  
Sbjct: 80725 cagatgtgtgaatactgcggatggtgaaggtggagcagtgatagcaacctgtgcaacca 80666

Query: 3282 ggatgaaattccccccagaaacccagtcctgttctcttatgtgtcccaatgagtggtgcat 3341  
|||||  
Sbjct: 80665 ggatgaaattccccccagaaacccagtcctgttctcttatgtgtcccaatgagtggtgcat 80606

Query: 3342 gtctgagtgaggactttggagcaaagtcacacag 3375  
|||||  
Sbjct: 80605 gtctgagtgaggactttggagcaaagtcacacag 80572

Score = 295 bits (149), Expect = 1e-76  
Identities = 149/149 (100%)  
Strand = Plus / Minus

Query: 3750 aggtcgaatgagccggactcgatttatcattatgccaaaccaaggagaaggacggccatg 3809  
|||||  
Sbjct: 10642 aggtcgaatgagccggactcgatttatcattatgccaaaccaaggagaaggacggccatg 10583

Query: 3810 cccacagagcttaccaggagaaaacctgccagtgacccccctgctacagctgggtcct 3869  
|||||  
Sbjct: 10582 cccacagagcttaccaggagaaaacctgccagtgacccccctgctacagctgggtcct 10523

Query: 3870 tggcaactgggtctgcatgtaaattggagg 3898  
|||||  
Sbjct: 10522 tggcaactgggtctgcatgtaaattggagg 10494

Score = 285 bits (144), Expect = 1e-73  
Identities = 144/144 (100%)  
Strand = Plus / Minus

Query: 3374 agtcatgcatccccacacaatgcagagaagaactcgccacctgctaagaccatcactga 3433  
|||||  
Sbjct: 36955 agtcatgcatccccacacaatgcagagaagaactcgccacctgctaagaccatcactga 36896

Query: 3434 actcaaggacttgtgctgaagactcacaggtgcagccttgccctcctgaatgaaaattgct 3493  
|||||  
Sbjct: 36895 actcaaggacttgtgctgaagactcacaggtgcagccttgccctcctgaatgaaaattgct 36836

Query: 3494 tccagttccagtacaatctaacag 3517  
|||||  
Sbjct: 36835 tccagttccagtacaatctaacag 36812

Score = 281 bits (142), Expect = 2e-72  
Identities = 145/146 (99%)  
Strand = Plus / Minus

Query: 3088 caggtacatgaggcagtcocatgttacagtgagtgcaatcagtattcctgggtttagaa 3147  
|||||  
Sbjct: 89910 caggtacatgaggcagtcocatgttacagtgagtgcaatcagtattcctgggtttagaa 89851

Query: 3148 cactggtcttcatgcaaaatcaacaatgagctgaggtccctgcgctgtggaggaggaaca 3207  
|||||  
Sbjct: 89850 cactggtcttcatgcaaaatcaacaatgagctgaggtccctgcgctgtggaggaggaaca 89791

Query: 3208 caatctaggaaaatcagatgtgtgaa 3233  
|||||  
Sbjct: 89790 caatctaggaaaatcaggtgtgtgaa 89765

Score = 246 bits (124), Expect = 1e-61  
Identities = 124/124 (100%)  
Strand = Plus / Minus

Query: 3630 gcagcataatttggagaagccccagagaatgagcattccctgcttggtggaatgcgtggt 3689  
|||||  
Sbjct: 32523 gcagcataatttggagaagccccagagaatgagcattccctgcttggtggaatgcgtggt 32464

Query: 3690 caactgtcagctctcaggggtggacggccttgacagagtgttcacagacctgtggccatgg 3749  
|||||  
Sbjct: 32463 caactgtcagctctcaggggtggacggccttgacagagtgttcacagacctgtggccatgg 32404

Query: 3750 aggt 3753  
|||  
Sbjct: 32403 aggt 32400

Score = 234 bits (118), Expect = 4e-58  
Identities = 118/118 (100%)  
Strand = Plus / Minus

Query: 3516 agagtggagcacatgccagctgagtgaaaacgcaccctgtggtcaaggcgtcaggaccgg 3575  
|||||  
Sbjct: 34738 agagtggagcacatgccagctgagtgaaaacgcaccctgtggtcaaggcgtcaggaccgg 34679

Query: 3576 cctgctaagctgtgtgtgcagtgatggcaagccagtcagcatggaccaatgtgagcag 3633  
|||||  
Sbjct: 34678 cctgctaagctgtgtgtgcagtgatggcaagccagtcagcatggaccaatgtgagcag 34621

>AC010873.12.1.180602  
Length = 180602

Score = 184 bits (93), Expect = 3e-43  
Identities = 93/93 (100%)  
Strand = Plus / Minus

Query: 1 atgaggaagctctttctattgctttctctcttgctgtcccatgcagctcatttgggaaggc 60  
|||||  
Sbjct: 107913 atgaggaagctctttctattgctttctctcttgctgtcccatgcagctcatttgggaaggc 107854

Query: 61      aaaaaggataatcagttcatctggaaaccaggt 93  
                 |||||  
Sbjct: 107853 aaaaaggataatcagttcatctggaaaccaggt 107821

Query= SEQ ID NO:5  
(4821 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AC011231.7.1.119205	<u>1612</u>	0.0
AC019067.9.1.169928	<u>535</u>	e-149
AC012000.3.1.194472	<u>470</u>	e-129
AC016679.9.1.89212	<u>387</u>	e-104
AC017082.4.1.183783	<u>305</u>	1e-79
AC010873.12.1.180602	<u>280</u>	8e-72

>AC011231.7.1.119205  
Length = 119205

Score = 1612 bits (813), Expect = 0.0  
Identities = 813/813 (100%)  
Strand = Plus / Minus

Query: 138 aggtccgtggggaaggtgtacaggagactgtggtcccgaggagtcagagtcgggcagt 197  
|||||  
Sbjct: 52727 aggtccgtggggaaggtgtacaggagactgtggtcccgaggagtcagagtcgggcagt 52668

Query: 198 gtggtgttttcatgttgacgggtggacaagtcacctgtctaactgtggtgagagcaacag 257  
|||||  
Sbjct: 52667 gtggtgttttcatgttgacgggtggacaagtcacctgtctaactgtggtgagagcaacag 52608

Query: 258 gcctccaaaggaaagaagttgtttccgagtttgtgactggcacagtgacctctttcagtg 317  
|||||  
Sbjct: 52607 gcctccaaaggaaagaagttgtttccgagtttgtgactggcacagtgacctctttcagtg 52548

Query: 318 ggagggtttctgactggcaccactgtgtgcttggttccttacgctcgcggtgaagtcaagcc 377  
|||||  
Sbjct: 52547 ggagggtttctgactggcaccactgtgtgcttggttccttacgctcgcggtgaagtcaagcc 52488

Query: 378 tcggactgcagagtgtgtgacggctcagcatggactgcagcaccggatggtgcgctgcat 437  
|||||  
Sbjct: 52487 tcggactgcagagtgtgtgacggctcagcatggactgcagcaccggatggtgcgctgcat 52428

Query: 438 tcagaagctgaaccgaactgtggttgcaaataaaatgcaaacactttgcccttcagcc 497  
|||||  
Sbjct: 52427 tcagaagctgaaccgaactgtggttgcaaataaaatgcaaacactttgcccttcagcc 52368

Query: 498 tcctacagaacaggcttgccctattccttggtccccgggattgtgtagtatctgagttctt 557  
|||||  
Sbjct: 52367 tcctacagaacaggcttgccctattccttggtccccgggattgtgtagtatctgagttctt 52308

Query: 558 accatgggtccaactgtagcaagggatgtgggaagaaattgcagcatagaactcgcgcggt 617  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 52307 accatgggtccaactgtagcaagggatgtgggaagaaattgcagcatagaactcgcgcggt 52248

Query: 618 catagctccccctctctttgggtgggttgcaatgtccaaatctgactgagtcaagagcctg 677  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 52247 catagctccccctctctttgggtgggttgcaatgtccaaatctgactgagtcaagagcctg 52188

Query: 678 tgatgctcccatttctctgtcctcttggggaagaggaatatacatttagccttaaggttgg 737  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 52187 tgatgctcccatttctctgtcctcttggggaagaggaatatacatttagccttaaggttgg 52128

Query: 738 accatggagtaaatagcagactgcctcatcttaaagaaattaatccaagcggaagaactgt 797  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 52127 accatggagtaaatagcagactgcctcatcttaaagaaattaatccaagcggaagaactgt 52068

Query: 798 tctggatttttaactctgattcaaatagagcgagtcacctttaaacatcaaagttacaaagc 857  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 52067 tctggatttttaactctgattcaaatagagcgagtcacctttaaacatcaaagttacaaagc 52008

Query: 858 acatcatcattcgaagtcttgggcaatagagataggttatcaaaccggcagggtttcgtg 917  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 52007 acatcatcattcgaagtcttgggcaatagagataggttatcaaaccggcagggtttcgtg 51948

Query: 918 tacaagaagtgatggacaaaatgctatgttaag 950  
||||||||||||||||||||||||||||||||  
Sbjct: 51947 tacaagaagtgatggacaaaatgctatgttaag 51915

Score = 507 bits (256), Expect = e-140  
Identities = 256/256 (100%)  
Strand = Plus / Minus

Query: 949 agcctttgccttcaagattccttcccattgactgttcagtcctgcatcatgccccaaagac 1008  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 14274 agcctttgccttcaagattccttcccattgactgttcagtcctgcatcatgccccaaagac 14215

Query: 1009 tgtgaaacctcccagtggtcctcctggagccccctgctccaagacatgccgttcagggagt 1068  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 14214 tgtgaaacctcccagtggtcctcctggagccccctgctccaagacatgccgttcagggagt 14155

Query: 1069 ctcttgccaggatttaggagcaggagccggaacgtgaagcacatggctattggaggtgga 1128  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 14154 ctcttgccaggatttaggagcaggagccggaacgtgaagcacatggctattggaggtgga 14095

Query: 1129 aaggagtgtcctgaacttcttgagaaagaggcctgcattggtgaaggagaacttctgcag 1188  
|||||  
Sbjct: 14094 aaggagtgtcctgaacttcttgagaaagaggcctgcattggtgaaggagaacttctgcag 14035

Query: 1189 caatgtcccaggtatt 1204  
|||||  
Sbjct: 14034 caatgtcccaggtatt 14019

>AC019067.9.1.169928  
Length = 169928

Score = 535 bits (270), Expect = e-149  
Identities = 270/270 (100%)  
Strand = Plus / Minus

Query: 2692 acagggaaaagcagaaagaaggagaaatgccaggattctgacctttaccctctagtggag 2751  
|||||  
Sbjct: 59740 acagggaaaagcagaaagaaggagaaatgccaggattctgacctttaccctctagtggag 59681

Query: 2752 acagaactatgtccttgtgatgaatttatatcccaaccttatggaaactggtcagattgc 2811  
|||||  
Sbjct: 59680 acagaactatgtccttgtgatgaatttatatcccaaccttatggaaactggtcagattgc 59621

Query: 2812 attcttccagaaggcagaagggagcctcaccgaggactgcgggtacaagcagacagcaaa 2871  
|||||  
Sbjct: 59620 attcttccagaaggcagaagggagcctcaccgaggactgcgggtacaagcagacagcaaa 59561

Query: 2872 gaatgtggagaaggcctgcgctttcgagcagtagcctgttctgataaaaaatggaagacct 2931  
|||||  
Sbjct: 59560 gaatgtggagaaggcctgcgctttcgagcagtagcctgttctgataaaaaatggaagacct 59501

Query: 2932 gttgacccctccttctgcagcagctctggt 2961  
|||||  
Sbjct: 59500 gttgacccctccttctgcagcagctctggt 59471

Score = 392 bits (198), Expect = e-106  
Identities = 198/198 (100%)  
Strand = Plus / Minus

Query: 2499 agctgtctcatgcatctctgatgacaaccgggtcagcagaaatgatggaatgcctcaagca 2558  
|||||  
Sbjct: 65734 agctgtctcatgcatctctgatgacaaccgggtcagcagaaatgatggaatgcctcaagca 65675

Query: 2559 gacaaacggcatgcctctccttgtgcaagaatgcacagtcccatgtcgagaagactgcac 2618  
|||||  
Sbjct: 65674 gacaaacggcatgcctctccttgtgcaagaatgcacagtcccatgtcgagaagactgcac 65615

Query: 2619 cttcactgcttgggtccaagtttacgccctgctccacgaactgtgaagccacaaaaagtag 2678  
|||||  
Sbjct: 65614 cttcactgcttgggtccaagtttacgccctgctccacgaactgtgaagccacaaaaagtag 65555

Query: 2679 gcggcgacagctcacagg 2696  
|||||  
Sbjct: 65554 gcggcgacagctcacagg 65537

Score = 363 bits (183), Expect = 7e-97  
Identities = 183/183 (100%)  
Strand = Plus / Minus

Query: 2959 ggttacattcaagaaaaatgtgtcattccctgcccatgtgattgcaagttaagcgattgg 3018  
|||||  
Sbjct: 20501 ggttacattcaagaaaaatgtgtcattccctgcccatgtgattgcaagttaagcgattgg 20442

Query: 3019 tctagttgggggtccttgcaagttcatcttgtggaattggagtgagaattcgatccaaatgg 3078  
|||||  
Sbjct: 20441 tctagttgggggtccttgcaagttcatcttgtggaattggagtgagaattcgatccaaatgg 20382

Query: 3079 ctaaaagaaaaaccttacaatggaggacgaccatgtcccaaactggatctcaagaatcag 3138  
|||||  
Sbjct: 20381 ctaaaagaaaaaccttacaatggaggacgaccatgtcccaaactggatctcaagaatcag 20322

Query: 3139 gta 3141  
|||  
Sbjct: 20321 gta 20319

>AC012000.3.1.194472  
Length = 194472

Score = 470 bits (237), Expect = e-129  
Identities = 237/237 (100%)  
Strand = Plus / Minus

Query: 1914 aggtggaaagccatgtccccctagtcaggctctccaagagcatcgtttgtgtaatgacca 1973  
|||||  
Sbjct: 70520 aggtggaaagccatgtccccctagtcaggctctccaagagcatcgtttgtgtaatgacca 70461



Query: 1974 ttctgtatgcagcttcactgggagacatcgccctggggcccttggtctgaggacacatt 2033  
|||||  
Sbjct: 70460 ttctgtatgcagcttcactgggagacatcgccctggggcccttggtctgaggacacatt 70401

Query: 2034 ggtaactgcccttaatgcaaccattggctggaatggagaagccacgtgtggtgtaggcat 2093  
|||||  
Sbjct: 70400 ggtaactgcccttaatgcaaccattggctggaatggagaagccacgtgtggtgtaggcat 70341

Query: 2094 tcagactcggagagtcttctgtgtcaagagtcacgtgggacaagtaatgacccaaaag 2150  
|||||  
Sbjct: 70340 tcagactcggagagtcttctgtgtcaagagtcacgtgggacaagtaatgacccaaaag 70284

Score = 398 bits (201), Expect = e-107  
Identities = 201/201 (100%)  
Strand = Plus / Minus

Query: 1524 aggatttagaacgaggcagcgccatgtcctcatggaatctacagggcctgcagggcattg 1583  
|||||  
Sbjct: 132678 aggatttagaacgaggcagcgccatgtcctcatggaatctacagggcctgcagggcattg 132619

Query: 1584 ccctcatttggtggagtctgttccttgtaggatccaatgtgctaccgatggctggcatc 1643  
|||||  
Sbjct: 132618 ccctcatttggtggagtctgttccttgtaggatccaatgtgctaccgatggctggcatc 132559

Query: 1644 agaagggatctgtttccctgatcatggaaaatgtggcctgggacatcgtattctgaaggc 1703  
|||||  
Sbjct: 132558 agaagggatctgtttccctgatcatggaaaatgtggcctgggacatcgtattctgaaggc 132499

Query: 1704 cgtctgccagaatgaccgcgg 1724  
|||||  
Sbjct: 132498 cgtctgccagaatgaccgcgg 132478

Score = 389 bits (196), Expect = e-104  
Identities = 196/196 (100%)  
Strand = Plus / Minus

Query: 1723 ggagaagatgtatcagggagtctttgccagttccccctcctcctgagaggaagtcttgt 1782  
|||||  
Sbjct: 72374 ggagaagatgtatcagggagtctttgccagttccccctcctcctgagaggaagtcttgt 72315

Query: 1783 gaaattccctgccgaatggactgtgtgctgagcgagtgagcgagtggtcatcctgttcc 1842  
|||||  
Sbjct: 72314 gaaattccctgccgaatggactgtgtgctgagcgagtgagcgagtggtcatcctgttcc 72255

Query: 1843 cagtcctgtttcaaataaaaaactcagatgggaaacagaccaggtcaagaactatcctggca 1902  
|||||  
Sbjct: 72254 cagtcctgtttcaaataaaaaactcagatgggaaacagaccaggtcaagaactatcctggca 72195

Query: 1903 ctggctggggaaggtg 1918  
|||||  
Sbjct: 72194 ctggctggggaaggtg 72179

Score = 343 bits (173), Expect = 6e-91  
Identities = 173/173 (100%)  
Strand = Plus / Minus

Query: 1197 caggtattcctgggagaacttctgaatggaaagaatgccaaagtctctctcctcctcgagca 1256  
|||||  
Sbjct: 188296 caggtattcctgggagaacttctgaatggaaagaatgccaaagtctctctcctcctcgagca 188237

Query: 1257 gcaggatccccactggcatgtgacgggacccgtgtgtggcggtgggatccagacccggga 1316  
|||||  
Sbjct: 188236 gcaggatccccactggcatgtgacgggacccgtgtgtggcggtgggatccagacccggga 188177

Query: 1317 ggtgtactgtgcccagagcgtaccagcagctgccgcactgagggccaaggaag 1369  
|||||  
Sbjct: 188176 ggtgtactgtgcccagagcgtaccagcagctgccgcactgagggccaaggaag 188124

Score = 307 bits (155), Expect = 3e-80  
Identities = 158/159 (99%)  
Strand = Plus / Minus

Query: 1368 agtctctagacctgtggaaaaggcattatgtgtgggacccgccccgttgccctctcagct 1427  
|||||  
Sbjct: 143206 agtctctagacctgtggaaaaggcattatgtgtgggacccgccccgttgccctctcagct 143147

Query: 1428 ctgcaatatcccttgctctacggactgcatagtatcttcctggtcagcctggggcctgtg 1487  
|||||  
Sbjct: 143146 ctgcaatatcccttgctctacggactgcatagtatcttcctggtcagcctggggcctgtg 143087

Query: 1488 catccatgaaaactgtcatgaacctcaggggaaaaaagg 1526  
|||||  
Sbjct: 143086 catccatgaaaactgtcatgatcctcaggggaaaaaagg 143048

Score = 266 bits (134), Expect = 1e-67  
Identities = 134/134 (100%)  
Strand = Plus / Minus

Query: 2264 caggaaatgccacagtaaaacagtctcgatacagaatcatcatccaagaagcagccaatg 2323  
|||||  
Sbjct: 30887 caggaaatgccacagtaaaacagtctcgatacagaatcatcatccaagaagcagccaatg 30828

Query: 2324 gaggccaggaatgccagataccttatatgaggagagagagtgtgaagatgtttccttgt 2383  
|||||  
Sbjct: 30827 gaggccaggaatgccagataccttatatgaggagagagagtgtgaagatgtttccttgt 30768

Query: 2384 gtcctgtatatcgg 2397  
|||||  
Sbjct: 30767 gtcctgtatatcgg 30754

Score = 236 bits (119), Expect = 1e-58  
Identities = 119/119 (100%)  
Strand = Plus / Minus

Query: 2149 agatgtccagattctactcgacctgaaactgtgcgccccctgttttctcccatgcaaaaaa 2208  
|||||  
Sbjct: 60962 agatgtccagattctactcgacctgaaactgtgcgccccctgttttctcccatgcaaaaaa 60903

Query: 2209 gactgtattgtgactgctttcagtgagtggacaccctgccaaggatgtgccaagcagg 2267  
|||||  
Sbjct: 60902 gactgtattgtgactgctttcagtgagtggacaccctgccaaggatgtgccaagcagg 60844

Score = 208 bits (105), Expect = 2e-50  
Identities = 105/105 (100%)  
Strand = Plus / Minus

Query: 2396 ggtggaagccacagaaatggagcccttgcatcttagtgccagagtctgtctggcagggaa 2455  
|||||  
Sbjct: 27495 ggtggaagccacagaaatggagcccttgcatcttagtgccagagtctgtctggcagggaa 27436

Query: 2456 taacgggcagcagtgaagcctgtggaaaggggttacaacaagag 2500  
|||||  
Sbjct: 27435 taacgggcagcagtgaagcctgtggaaaggggttacaacaagag 27391

>AC016679.9.1.89212

Length = 89212

Score = 387 bits (195), Expect = e-104

Identities = 195/195 (100%)

Strand = Plus / Plus

Query: 4457 aggggtggagtctgtggttgtgagaagggctatacagagataatgaaatcaaattgggtttcc 4516  
|||||

Sbjct: 12254 aggggtggagtctgtggttgtgagaagggctatacagagataatgaaatcaaattgggtttcc 12313

Query: 4517 tggattactgcatgaaagtaccaggctcagaggataaaaaagctgatgtgaaaaaccttt 4576  
|||||

Sbjct: 12314 tggattactgcatgaaagtaccaggctcagaggataaaaaagctgatgtgaaaaaccttt 12373

Query: 4577 ctgggaaaaacagacctgtgaattcaaaaatacatgatatttttaaggatgggtctcttc 4636  
|||||

Sbjct: 12374 ctgggaaaaacagacctgtgaattcaaaaatacatgatatttttaaggatgggtctcttc 12433

Query: 4637 aaccacttgatccag 4651  
|||||

Sbjct: 12434 aaccacttgatccag 12448

Score = 355 bits (179), Expect = 2e-94

Identities = 179/179 (100%)

Strand = Plus / Plus

Query: 4102 ccaggagactgccatttaacagaatgggtcagagtggagcacatgtgaattaacctgcatt 4161  
|||||

Sbjct: 5665 ccaggagactgccatttaacagaatgggtcagagtggagcacatgtgaattaacctgcatt 5724

Query: 4162 gatggaagaagctttgagactgtgggccgccagtctagatcaaggacttttataattcag 4221  
|||||

Sbjct: 5725 gatggaagaagctttgagactgtgggccgccagtctagatcaaggacttttataattcag 5784

Query: 4222 tcttttgagaaccaagacagctgcccccaacagggttctagaaacacgcccttgtagagg 4280  
|||||

Sbjct: 5785 tcttttgagaaccaagacagctgcccccaacagggttctagaaacacgcccttgtagagg 5843

Score = 323 bits (163), Expect = 6e-85  
Identities = 163/163 (100%)  
Strand = Plus / Plus

Query: 3944 aggggtggagactgtggggaaggagttcagatccgcagcctttcctgcatgggtccacagtg 4003  
|||||  
Sbjct: 4372 aggggtggagactgtggggaaggagttcagatccgcagcctttcctgcatgggtccacagtg 4431

Query: 4004 gttcaatatctcatgcagctggacgtgtcgaggatgcactgtgtggagaaatgccctttc 4063  
|||||  
Sbjct: 4432 gttcaatatctcatgcagctggacgtgtcgaggatgcactgtgtggagaaatgccctttc 4491

Query: 4064 aggacagcatcctgaagcagctgtgttctgtgccttgcccagg 4106  
|||||  
Sbjct: 4492 aggacagcatcctgaagcagctgtgttctgtgccttgcccagg 4534

Score = 202 bits (102), Expect = 1e-48  
Identities = 102/102 (100%)  
Strand = Plus / Plus

Query: 4275 tacaggaggcaaatgttatcactacacatggaaagcaagtctttggaacaataacgaacg 4334  
|||||  
Sbjct: 5933 tacaggaggcaaatgttatcactacacatggaaagcaagtctttggaacaataacgaacg 5992

Query: 4335 aactgtatggtgccagcggttcagatggcggttaatgtcacagg 4376  
|||||  
Sbjct: 5993 aactgtatggtgccagcggttcagatggcggttaatgtcacagg 6034

Score = 180 bits (91), Expect = 5e-42  
Identities = 91/91 (100%)  
Strand = Plus / Plus

Query: 4649 cagatggccgagtaaaaaatttgggtttatggcgtttcaggtggcgcttttctcatcatga 4708  
|||||  
Sbjct: 16644 cagatggccgagtaaaaaatttgggtttatggcgtttcaggtggcgcttttctcatcatga 16703

Query: 4709 ttttcctaataatttacttcctaccttggttg 4739  
|||||  
Sbjct: 16704 ttttcctaataatttacttcctaccttggttg 16734

Score = 172 bits (87), Expect = 1e-39  
Identities = 87/87 (100%)  
Strand = Plus / Plus

Query: 4373 caggaggctgctcccctcaggcccgtcctgctgccattcggcagtgcatccagcctgca 4432  
|||||  
Sbjct: 8534 caggaggctgctcccctcaggcccgtcctgctgccattcggcagtgcatccagcctgca 8593

Query: 4433 gaaaacctttctcctactgtacacagg 4459  
|||||  
Sbjct: 8594 gaaaacctttctcctactgtacacagg 8620

Score = 165 bits (83), Expect = 3e-37  
Identities = 83/83 (100%)  
Strand = Plus / Plus

Query: 4739 gcaagaagccaaaaccacatcaaagcacacctccccaacagaagcctctgaccttagcct 4798  
|||||  
Sbjct: 25396 gcaagaagccaaaaccacatcaaagcacacctccccaacagaagcctctgaccttagcct 25455

Query: 4799 acgatggagacttagacatgtaa 4821  
|||||  
Sbjct: 25456 acgatggagacttagacatgtaa 25478

>AC017082.4.1.183783  
Length = 183783

Score = 305 bits (154), Expect = 1e-79  
Identities = 154/154 (100%)  
Strand = Plus / Minus

Query: 3270 cagatgtgtgaatactgcggatggtgaaggtggagcagtgatagcaacctgtgcaacca 3329  
|||||  
Sbjct: 80725 cagatgtgtgaatactgcggatggtgaaggtggagcagtgatagcaacctgtgcaacca 80666

Query: 3330 ggatgaaattccccagaaacccagtcctgttctcttatgtgtcccaatgagtggtgcat 3389  
|||||  
Sbjct: 80665 ggatgaaattccccagaaacccagtcctgttctcttatgtgtcccaatgagtggtgcat 80606

Query: 3390 gtctgagtgagggactttggagcaaatgccacag 3423  
|||||  
Sbjct: 80605 gtctgagtgagggactttggagcaaatgccacag 80572

Score = 295 bits (149), Expect = 1e-76  
Identities = 149/149 (100%)  
Strand = Plus / Minus

Query: 3798 aggtcgaatgagccggactcgatttatcattatgccaaaccaaggagaaggacggccatg 3857  
|||||  
Sbjct: 10642 aggtcgaatgagccggactcgatttatcattatgccaaaccaaggagaaggacggccatg 10583

Query: 3858 cccacagagcttaccaggagaaaacctgccagtgacccccctgctacagctgggtcct 3917  
|||||  
Sbjct: 10582 cccacagagcttaccaggagaaaacctgccagtgacccccctgctacagctgggtcct 10523

Query: 3918 tggcaactgggtctgcatgtaaattggagg 3946  
|||||  
Sbjct: 10522 tggcaactgggtctgcatgtaaattggagg 10494

Score = 285 bits (144), Expect = 1e-73  
Identities = 144/144 (100%)  
Strand = Plus / Minus

Query: 3422 agtcatgcatccccacacaatgcagagaagaactcgccacctgctaagaccatcactga 3481  
|||||  
Sbjct: 36955 agtcatgcatccccacacaatgcagagaagaactcgccacctgctaagaccatcactga 36896

Query: 3482 actcaaggacttgtgctgaagactcacaggtgcagccttgccctcctgaatgaaaattgct 3541  
|||||  
Sbjct: 36895 actcaaggacttgtgctgaagactcacaggtgcagccttgccctcctgaatgaaaattgct 36836

Query: 3542 tccagttccagtacaatctaacag 3565  
|||||  
Sbjct: 36835 tccagttccagtacaatctaacag 36812

Score = 281 bits (142), Expect = 2e-72  
Identities = 145/146 (99%)  
Strand = Plus / Minus

Query: 3136 caggtacatgaggcagtcctcatgttacagtgagtgcaatcagtattcctgggtttagaa 3195  
|||||  
Sbjct: 89910 caggtacatgaggcagtcctcatgttacagtgagtgcaatcagtattcctgggtttagaa 89851

Query: 3196 cactggtcttcatgcaaaatcaacaatgagctgaggtccctgcgctgtggaggaggaaca 3255  
|||||  
Sbjct: 89850 cactggtcttcatgcaaaatcaacaatgagctgaggtccctgcgctgtggaggaggaaca 89791

Query: 3256 caatctaggaaaatcagatgtgtgaa 3281  
|||||||  
Sbjct: 89790 caatctaggaaaatcaggtgtgtgaa 89765

Score = 246 bits (124), Expect = 1e-61  
Identities = 124/124 (100%)  
Strand = Plus / Minus

Query: 3678 gcagcataatttgagagaagccccagagaatgagcattccctgcttggtggaatgcgtggt 3737  
|||||||  
Sbjct: 32523 gcagcataatttgagagaagccccagagaatgagcattccctgcttggtggaatgcgtggt 32464

Query: 3738 caactgtcagctctcaggggtggacggcttgacagagtgttcacagacctgtggccatgg 3797  
|||||||  
Sbjct: 32463 caactgtcagctctcaggggtggacggcttgacagagtgttcacagacctgtggccatgg 32404

Query: 3798 aggt 3801  
||||  
Sbjct: 32403 aggt 32400

Score = 234 bits (118), Expect = 4e-58  
Identities = 118/118 (100%)  
Strand = Plus / Minus

Query: 3564 agagtggagcacatgccagctgagtgaaaacgcaccctgtggtcaaggcgtcaggaccg 3623  
|||||||  
Sbjct: 34738 agagtggagcacatgccagctgagtgaaaacgcaccctgtggtcaaggcgtcaggaccg 34679

Query: 3624 cctgctaagctgtgtgtgcagtgatggcaagccagtcagcatggaccaatgtgagcag 3681  
|||||||  
Sbjct: 34678 cctgctaagctgtgtgtgcagtgatggcaagccagtcagcatggaccaatgtgagcag 34621

>AC010873.12.1.180602  
Length = 180602

Score = 280 bits (141), Expect = 8e-72  
Identities = 141/141 (100%)  
Strand = Plus / Minus

Query: 1 atgtttccaaagagcaacctaacagtcacttgctgggtatggaggagcatgaggaagctc 60  
|||||||  
Sbjct: 107961 atgtttccaaagagcaacctaacagtcacttgctgggtatggaggagcatgaggaagctc 107902



Query: 61 tttctattgcttttctctcttgctgtcccatgcagctcatttggaaggcaaaaaggataat 120  
|||||  
Sbjct: 107901 tttctattgcttttctctcttgctgtcccatgcagctcatttggaaggcaaaaaggataat 107842

Query: 121 cagttcatctggaaaccaggt 141  
|||||  
Sbjct: 107841 cagttcatctggaaaccaggt 107821